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GenCore version 5.1.6
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OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	September 18, 2004, 09:46:06; Search time 1142.55 Seconds (without alignments) 9066.559 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-614-282-1 239 1 atcagtcacgacttggtaagtgtggttccggctggacaat 239
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	3470272 seqs, 21671516995 residues
Total number of	Total number of hits satisfying chosen parameters: 6940544

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : GenEmbl:*

Minimum DB seq length: 0
Maximum DB seq length: 200000000

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GenEmbl:* gb_ba: gb_htg: gb_in: gb_om: gb_ow: gb_ov: gb_pat: gb_pat: gb_pat: gb_pat:		
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT 1 DMIABG1 LOCUS DEFINITION ACCESSION VERSION	DMLABG1 1846 bp DNA linear INV 06-OCT-1999 Drosophila melanogaster lab gene for labial protein, exon 1 and joined CDS. X13104 X12834 X13104.1 G1:8171
KEYWORDS SOURCE ORGANISM	alternative splicing; antennapedia complex; homeobox; lab gene. Drosophila melanogaster (fruit fly) Drosophila melanogaster Drosophila melanogaster Drosophila melanogaster
REFERENCE AUTHORS	<pre>buxalyous, metazon, Attnicopous, Hexapous, Lisecta; Fleiygota; Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae; Drosophila. 1 (bases 1 to 1846) Mlodzik,M., Fjose,A. and Gehring,W.J.</pre>

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KEYWORDS
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OPHLOLOCOCOHCHLOOPCOHLTYNOYTESSFEWTYPOCACOLTPPPTSHPOOH
OQCACOCOLTPHSHLPS PARAEVET TITSTTTCHPGKPLHPSSHSPADSYTESDSWHS
YYATAYTYA PPSINSSPITAANASATSNYCOCOCOAL IS SENGMYTNLLCTWYPT
OAQAPUHGYAGOIE EKYAAVLHASYAPGWYLEDOLPPMQQATOSOWHQPOHODPHOOT
DAMBOLLGMAHMHHGLIPHGHLGNLLANNPHQQOPQOPQOPQOPHQDPHOONSYAAV
COCHAONSVSPWGGMANROCORGY SPGSSTSSSTSSANGAHPASTOSKSPAHH
OCHHONSVSPWGGMANROCORGY SPGSSTSSSTSSANGAHPASTOSKSPAHSSSIPTY
KWMQLKRNVFKPQAPSYLPAPKLPASGIASMHDYQMNGQLDMCRGGGGGSDVGSPV
GGGGGGGGGGGGGSLTMANSAAAGSAHPMOMOVGLGGGGGGSSCLSSNYNN
SGRTNFTNKOLIFELEKEPHFNYLTRARR IE TANTLOLNBTOWRINFRONKRKKY
KEGLIPALLTQHSTSVISEKPPROQOPOPPELQLKSQCSDLGGNELATRA
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QAQAPVHGYAGQIEEKYAAVLHASYAPGWVLEDQDPMMQQATQSQMWHQQHLAGSYA
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QQHHQNSVSPNGGMNRQQRGGVISPGSSTSSSTSASNGAHPASTQSKSPNHSSSIPTY
KWMQLKRNVPKPQAPKLPASGIASMHDYQMNGQLDMCRGGGGGGGSDVGSGPVGVGGNG
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TNKQLTELEKEFHFNRYLTRARRIEIANTLQLNETQVKINFQNRRMKQKKRVKEGLIP
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Molecular structure and spatial expression of a homeobox gene from the labial region of the Antennapedia-complex EMBO J. 7 (8), 2569-2578 (1988) 89052673
                                                                                                                                                                                                           Submitted (12-AUG-1988) Doelz R., Biocomputing Biozentrum der Universiteit, Klingelbergstrasse 70, CH-4056 Basel, Switzerland see M13570 for overlapping sequence.
Location/Qualifiers
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/gene="lab"
392. .1846
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join(631.
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ENVARIYORA, MEGAZORA, AFTINIOPOGA; HEXADOGA; LIBECCA; PICETYGORA; REAZOZA; AFTINIOPOGA; INEXADYPORA; PREAZOZA; AFTINIOPOGA; INEXADAGA ; LICALSON, J.; BDNYCTOIGER; DOSCOPHILIGAE; DROSCOPHILA.

Stapleton, M., Brokstein, P., Hong, L., Abbayani, A., Carlson, J.; Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E., George, R., Gonzalez, M., Guazin, H., Krommiller, B., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nano, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M. and Celhiker, S.

Direct Submission

AL Liavrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA

Sequence Submitted by:

Berkeley, CA 94720, USA

Sequence submitted by:

Berkeley, CA 94720

This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection I (Rubin et al., Science 2000). The sequence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to a couragely within 100 kb in the genome. Thus we believe the sequence that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcription of unspliced precursor RNAs, and reverse transcription et unit in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site changefulifily. Derkeley. edu) or send email to changefulifily. Derkeley. edu.
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                                                               TCGTGTTTTTCGGTTCGATACAGATAAAACCCACGTCGATAGCCCTCGACCGTCGCGTAA 120
                                                                                                                                                                                             121 TATTCTTAGAAAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGTGGCAAGTGAAGGGT 180
392 ATCAGTCACGACTTGGTAAGCGCGCAGGCAGCACGTCGTCGTCGTCATCGCCAACGGGAG 451
                                                                                                                                                                                                                                                                                                                        181 AGTTAGTGATACACCGGTTATATCGGAGTGGCGAGAAGTGTGGTTCCGGCTGGACAAT 239
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                                                                                                      Eukaryota; Metazož; Arthropoda; Hexapoda; Insecta; Pterygota;
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/db_xref="FLYBASE:FBgn0002552"
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/product="RE63854p"

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Conservative

Best Local Similarity

Matches 239; Query Match

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1 ATCAGTCACGACTTGGTAAGCGCGCAGCAGCACGTCGTCGTCGTCATCGCCAACGGGAG 60

100.0%; Score 239; DB 3; Length 1846; 100.0%; Pred. No. 2.5e-66;

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OQHHONSVSPNGGMNRQQRGGVISPGSSTSSSTSASNGAHPASTQSKSPNHSSSIPTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was identified as CDM:10212650 by the submitter. For more information on this record e-mail to fly@celera.com. * NOTE: This is a 'werking draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Bidopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (Bases I to 63442)
Adams, M. and Venter, J.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                       Score 239; DB 3;
Pred. No. 2.7e-66;
; Mismatches 0;
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/protein_id="AAM11417.1"
/db_xref="GI:20152115"
/db_xref="FLYBASE:FBgn0002522"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'mol_type="genomic DNA"
'db xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                         100.0%;
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HTG; HTGS_PHASE2.
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Best Local Similarity
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Matches 239; Conserv
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VERSION
KEYWORDS
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AC020280
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Indels

Mismatches

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239; Conservative

Matches

1 ATCAGTCACGACTTGGTAAGCGCGCAGGCAGCACGTCGTCGTCGTCGTCGCCAACGGGAG

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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;

Bphydroidea; Drosophilidae; Drosophila.

Ephydroidea; Drosophilidae; Drosophila.

I (bases 1 to 85757)

Syirskas, R.R., Harris, N.L., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, K.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Mok, M.S., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R., Zhang, R., Zieran, L.L., and Kimmel, B.

Sequencing of antennapedia complex, homeotic genes

Lu pupulished (1997)

1 (Asses 1 to 8577)
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For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://fruitfly.berkeley.edu/sequence/) or send email to drosophila@mhgc.lbl.gov.
                                                                                                                                                                                                                                                                                                                                                               7016
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                                              9689
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                                                                                                                                                                                                                                                                                                                                                                                                                                              239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC001652 85757 bp DNA linear INV 17-JUL-19:
Drosophila melanogaster DNA sequence (P1 DS00004 (D12)), complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCOLGES L76986 L32616 L46822 L81326 L79833 L32614 L81325 L42048 L79834 L46820 L32619 L43416 L32618 L32615 L42053 L42049 L42051 L42050 L76988 L42052 L76987 L81327 L32621 L46821 L32612 L43415 L76985 L79255 L32622 L32613 L32627 L32620 ACCOL652.1 GI:2341048
TCGTGTTTTTCGGTTCGATACAGATAAAACCCACGTCGATAGCCCTCGACCGTCGCGTAA
                                                                                                                                                                                                                                                                                    TATTCTTAGAAAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGTGGCAAGTGAAGGGT
                                                                                                                                                                                                                                                                                                                                                               6957 TATTCTTAGAAAGCAAACAAGCTAAAGAACTATTTCAAGAACTGTGTGGGCAAGTGAAGGGT
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
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Submitted (22-APR-1997)
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12410 TATTCTTAGAAAGCAAACAGCTAAACAACTATTTCAAGAACTGTGTGGGAAGTGAAGGT 12351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12530 ATCAGTCACGACTTGGTAAGCGCGCGCAGCACGTCGTCGTCGTCGTCGTCGCCAACGGGAG 12471
Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dotsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwan, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T. C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pétiffer, B., Phouanenavong, S., Pittman, G. S., Puri, V., Richards, S., Scheeler, F., Stappleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Sequencing of Drosophila chromosome 3R, region 83F-84A
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Drosophila melanogaster BAC library, partial BcoRI in
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/mol_type="denomic DNA"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
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100.0%; Pred. No. 5.5e-66;
ive 0; Mismatches 0;
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Best Local Similarity
Matches 239; Conserv
                                                                                                                                                                                                                                  TITLE
JOURNAL
REFERENCE
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 170801)
Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
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                                                                                                                                                 1 ATCAGTCACGACTTGGTAAGCGCGCAGGCAGGAGGTCGTCGTCGTCGTCATCGCCAACGGGAG
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                                                                Length 85757;
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                                                             100.0%; Score 239; DB 3; 100.0%; Pred. No. 4.9e-66;
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Pred. No. 5.1e-66;
                                                                                                        0; Mismatches
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    belonging to this clone."
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AE001572 1
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Continuation <sup>[4</sup> of
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AE001572_3
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AC095014/c
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12350 AGTTAGTGATACACCGGTTATATCGGAGTGGCGAGAAAGTGTGGTTCCGGCTGGACAAT 12292

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SOURCE

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Neopera; Endoperator, Action poor; Insecta; Freelysta; Recomprise Ephydroides; Drosophilidae; Drosophila.

Ephydroides; Drosophilidae; Drosophila.

I (bases 1 to 175648)

Celniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,

Gelniker,S.E., Adams,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C.,

Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A.,

Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,

Carlson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D.,

Ferriera,S., Frise,E., Galle,R.F., Gargy,N.S., George,R.A.,

Gonzalez,M., Houck,J., Hoskin,B., Howland,T.J.,

McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunco,J.,

Phouanenavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F.,

Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M.,

Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.,

Squencing of Drosophila chromosome 3R, region 83F-83F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Rolliker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Rolliker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Rogers, Y., An, H., Baldwin, D., Banzon, J., Beradon, R.Y.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,
Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskin, B., N.S., George, R.A.,
Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,
McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,
Pacleb, J., Paragas, V., Park, S., Patel, S., Feiffer, B.,
Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,
Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,
Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.
Direct Submission
L. Submitted (15-SEP-2001) Berkeley Drosophila Genome Project, MS
G4-121, Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA, 94720, US
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Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
This sequence was assembled using end sequences from a whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email
       Drosophila melanogaster, chromosome 3R, region 83F-83F, BAC clone ACR19114, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="RPCI-98 (Roswell Park Cancer Institute Drosophila melanogaster BAC library, partial EcoRI in
                                                                                                                                                                                                                                                       Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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/strain="y; on bw sp"
/db xref="taxon:7227"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'chromosome="3R"
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JOURNAL
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JOURNAL
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KEYWORDS
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COMMENT

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Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota, Endopterygota; Diptera; Brachycera; Muscomorpha;

Epydroidea; Drosophilade; Drosophila.

(bases 1 to 298020)

Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D.,

Amanatides, P.G., Scherer,S.E., Li,P.W., Hoskhurner,M., Henderson,S.N.,

Sutcon,G.G., Wortman,J.R., Yandell,M.D., Zhang,O., Chen,L.X.,

Brandon,R.C., Rogers,Y.H., Blazaj,R.G., Champe,M., Pfeifer,B.D.,

Wan,K.H., Doyle,C., Baxert,E.G., Helt,G., Nelson,C.R., Galor,G.L.,

Abrill,J.F., Agbayani,A., An,H.J., Andrews-Pfannkoch,C., Bador,G.L.

Ballew,R.M., Basu,A., Baxendale,J., Bayraktaroglu,L., Beasley,E.M.

Ballew,R.M., Basm,D.A., Butler,H., Cadieu,E., Corteer,A.,

Burtis,K.C., Busam,D.A., Buller,H., Cadieu,E., Corteer,A.,

Daviss,P., Mebandos,B., Delcher,A., Dong,C., Mays,A.D., Dew,I.,

Dietz,S.M., Dodson,K., Doup,L.E., Downes,M., Dugar-Rocha,S.,

Dunkov,B.C., Punn,P., Durbin,K.J., Evangelista,C.C., Ferrac,C.,

Ferriera,S., Fleischmann,W., Fosler,C., Garzin,R.M., Harris,M., Houston,K.A., Howland,T.J.,

Wei,M.H., Ibegwam,C., Jalai,M., Kalush,F., Karpen,G.H., Ke,Z.,

Kravitz,S., Kulp,D., Lai,Z., Lasko,P., Lei,Y., Levitsky,A.,.

Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Mate,B., Moland,T.J.,

Muskern,D.R., Moshrefi,A., Mount,S.M., Moly,M., Murphy,B., Murphy,L.,

Muskern,D.R., Pacleb,J.M., Palazzolo,M., Pittman,G.S., Pan,S.,

Pollard,J., Puli,V., Resee,M.G., Reinert,K., Remington,K.,

Saunders,R.D., Saund, S., Shih, T., Spier,E., Spradling,A.C.,

Stapleton,M., Skups,R., Suh, H., Shih,T., Spier,E., Spradling,A.C.,

Stapleton,M., Skups,R., Shih,H., Shih, Saund, Saunders,R.D.,

Stapleton,M., Skups,R., Suh, R., San,R., Shan,R., Saunders,R.D., Saunders,R.D., Saunders,R.D., Saunders,R.D., Saunders,R.D., Saun
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                                                                                                                                                                                                                             144223 ATCAGTCACGACTTGGTAAGCGCGCAGCAGCACGTCGTCGTCGTCGTCGCCAACGGGAG 144164
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Drosophila melanogaster chromosome 3R, section 10 of 118 of the
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                                                                                                                                                                                                                                                                                                      61 TCGTGTTTTTCGGTTCGATACAGATAAAACCCACGTCGATAGCCCTCGACCGTCGCGTAA
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                                                                                    Gaps
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       Length 175648;
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Score 239; DB 3;
Pred. No. 5.5e-66;
; Mismatches 0;
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AE003674 AE002699 AE014297
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100.0%;
Query Match
Best Local Similarity 100.
Matches 239; Conservative
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KEYWORDS
SOURCE
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protein_id="AAF54118.1"
|db_xref="GI:7298912"
|db_xref="FLYBASE:FBgn0037448"
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/db_xref="FLYBASE:FBti0019320"
47311. .48339
                                                              .13156,13329. .14054)
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/gene="tRNA:M2:83F"
/locus_tag="CR31310"
/product="tRNA-Met"
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/gene="tRNA:M2:83F"
/locus_tag="CR31310"
                                                                                                                                                                 /product="CG15186-PA"
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/map="83F1-83F1"
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                                                                                                                                                                         Linker, S. L., Adams, M.D., Kronmiller, B., Wan, K.H., Holt, R.A.,
Bvans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y.,
Bvans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y.,
Banzon, J. An, H., Baldwin, D., Banzon, J., Beecon, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,
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Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
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McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,
Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,
Stapleton, M., Strong, R., Svirskas, R., Tector, C., Tyler, D.,
Williams, S.M., Zaveri, J.S., Smith, H.O., Venter, J.C. and Rubin, G.M.,
Sequencing of Drosophila melanogaster genome
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Submitted (O6-SBF-2002) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
6 (bases 1 to 298020)
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Submitted (13-FEB-2003) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
Sequence update by submitter
On Sep 18, 2002 this sequence version replaced gi:10727121.
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Mirar, S., Crosby, M.A., Matthews, B.B., Bayraktaroglu, L.,
Campbell, K., Hradecky, P., Huang, Y., Kaminker, J.S., Prochnik, S.E.,
Smith, C.D., Tupy, J.L., Bergman, C.M., Berman, B.P., Carlson, J.W.,
Celniker, S.E., Clamp, M.E., Drysdale, R.A., Emmert, D., Frise, E., de
Grey, A.D. N.J., Harris, N.L., Krommiller, B., Marshall, B.,
Milburn, G.H., Richter, J., Russo, S., Searle, S.M.J., Smith, E.,
Shu, S., Smutniak, F., Whitfield, E.J., Ashburner, M., Gelbart, W.M.,
Rubin, G.M., Mungall, C.J. and Lewis, S.E.
Annotation of Drosophila melanogaster genome
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... yenome sequence of Drosophila melanogaster Science 287 (5461), 2185-2195 (2000) 10731132
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CVDLSTVLTHPAIKAFKMSHSTPNSPHSSRRRTNSNSMSAPPGIPVSSGHPEVGATAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSHSHHHPHSGMVISSNPHHSHHSHQDSNHETVTSLSDRNSNSFASSRESSTSFSMRS
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APPSTTHHHHHRKEGSDPVPMTATVSRTKCSRRHSEGTVHTVHRNSAASGGAGGGHH
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NRRKISVSSHTGGKIPWCGCWGNGCL"
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Mizny, D. Marie., Met28cy, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, E., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Balderi, E., Baden, H., Baladaranaike, D., Barber, M., Baca, B., Baden, H., Baladaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chavez, D., Chen, Z., Chen, Z., Chen, Z., Char, Y., Chan, Z., Char, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., Davis, C., Dederich, D., Delgado, O., Denson, S., Dernon, C., Ding, Y., Dinh, H., Divya, K., Eraser, C.M., Escotto, M., Escotto, M., Edgene, C., Evans, C.A., Falls, T., Fan, G., Farser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, M., Guevara, W., Gunzarber, D., Haaland, W., Fladgo, M., Forbes, L., Foster, M., Guevara, W., Gunzarbe, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harrandez, S., Hadun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hladun, S.L., Hodgson, N., Hogues, M., Hollins, B., Howells, S., Hladun, S.L., King, L., Kovar, C., Kowis, C., Kraft, C.L., Jang, H., Johnson, R., Lou, W., Liu, W., Martine, R., Martine, R., Mapue, P., Martin, R., Martine, R., Mapue, P., Martin, R., Martine, S., Mullosavljevic, R., Martin, R., Martine, S., Mullosavljevic, R., Morris, R., Martin, N., Norris, S., Nachon, N., Norris, S., Nachon, N., Norris, S., Nachon, N., Norris, S., Nachon, N., Naurby, N., Naris, S., Nachon, N., Naurby, N., Naris, S., Nachon, N., Naris, S., Nachon, N., Naur
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Rattus norvegicus clone CH230-102113, WORKING DRAFT SEQUENCE, 3
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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note="last curated on Thu Jan 03 10:58:20 PST 2002"
map="83F1-83F1"
                                                                                                                                                                                                                    Length 298020;
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0; Mismatches 0;
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Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.

On May 13, 2003 this sequence version replaced gi:22857405.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlass (http://www.hgsc.bcm.tmc.ed/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contigs caffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequence and whole genome shotgun sequence reads.
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper. F., Poindexter A., Popovic, D., Primus, B., Pu, L. -L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Redger, M., Rachlin, E., Reeves, K., Redger, M., Rachlin, B., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Shartshar, S., Sher, F., Shett, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbey, A., Scherer, S., Sorelle, R., Soa, J., Shetty, J., Shvartsbey, A., Sisson, I., Sitter, C.D., Smajs, D., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, N., Tingey, A., Trejos, Z., Usmani, R., Valas, R., Valas, R., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Walcon, L., Walte, F., Willams, G., Willson, R., Wleck, M., Walco, L., Yoon, U., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Rat Genome Sequencing Consortium.
Direct Submission
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Worley, K.C.
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence It currently
consists of 3 contigs. The true order of the pieces
is not known and their order in this sequence record is Quality coverage: 8x in Q20 bases; sum-of-contigs estimation NOTE: Estimated insert size may differ from sequence length Consensus quality: 229128 bases at least Q40 Consensus quality: 231415 bases at least Q20 Consensus quality: 233051 bases at least Q20 Estimated insert size: 240583; sum-of-contigs estimation arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will 234954: contig of 234954 bp in length 235054: gap of unknown length 236441: contig of 1387 bp in length Center clone name: CH230-102113
------ Summary Statistics
Assembly program: Atlas 3.0; be preserved 234955 235055

Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu

---- Project Information

Center project name: GLTZ

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source
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215052 ATAGTTTTGGAAACCAAGCAACTAGATAATATTTTATCAACAGAGTGGAAATGCTAGAA 215111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC131194 239015 bp DNA linear HTG 10-MAY-2003 Rattus norvegicus clone CH230-85M5, WORKING DRAFT SEQUENCE. AC131194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 ATATTCTTAGAAAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGTGGCAAGTGAAGGG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 15.3%; Score 36.6; DB 2; Length 237630; Best Local Similarity 58.9%; Pred. No. 4.1; Matches 63; Conservative 0; Mismatches 44; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215112 TAGAGCATTÁGATGGCTGTGTTTTCTGAATGACAAGGAGTTCAGCTT 215158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 TAGTTAGTGATACACCGGTTATATCGGAGTGGCGAGAAAGTGTGGTT 226
2 236541: gap of unknown length
2 237630: contig of 1089 bp in length.
LocationQualifiers
1. .237630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG; HTGS PHASE2; HTGS DRAFT; HTGS FULLTOP Rattus norvegicus (Norway rat)
                                                                                                                                                   /organism="Rattus norvegicus"
                                                                                                                                                                                  /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                              1. .1505
/note="wgs_contig"
2205. .4409
                                                                                                                                                                                                                                                                                                                                                                                                       /note="wgs_contig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC131194.3 GI:30522034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 239015)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
                                      236542
                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                    source
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AC131194
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
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VERSION
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                                                                         FEATURES
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Nurany, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebeni, V., Aoyagi, A., Ayogaji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Blawalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Brante, C., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Carter, K., Cavazos, I., Casar, H., Center, A., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D. Sousa, D., Dengado, O., Denson, S., Derwn, A., Durbin, K., Duval, B., Eaves, K., Egan, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Derger, H., Dugan-Rocha, S., Durn, A., Durbin, K., Duval, B., Eaves, K., Egan, R. Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flaggon, V., Erbes, L., Foster, M., Geerra, W., Gabisi, A., Ganta, R., Gardy, M., Garza, M., Gabisi, A., Ganta, R., Gardy, M., Guerra, W., Gavara, W., Ghraer, C.M., Gabisi, A., Hadilon, C., Hamilton, C., Hamilton, K., Harnandez, R., Hawells, S., Hladun, S.L., Hodgoon, A., Hodgoon, A., Hodgoon, A., Hodgoon, A., Howells, S., Hladun, S.L., Hodgoon, M., Hernandez, M., Hanes, S., Hadun, S.L., Hodgoon, M., Lavis, L., Li, Z., Liu, J., Lui, W., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensulwa, L., Loulseqed, H., Lorado, R., Malloy, K., Mangum, A., Mahnen, P., Mangum, R., Mangum, R., Mangum, P., Mantin, R., Mangum, R., Mangum, B., Manua, P., Martin, R., Martin, R., Mangum, R., Mangum, R., Mangum, R., Mangum, P., McLeod, M.P., McNeill, T.Z., Meenen, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14324 ATAGTTTTGGAAACCAAGCAACTAGATAATATTTATCAACAGAGTGGAAATGCTAGAA 14383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG 10-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 ATAITCTTAGAAAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGTGGCAAGTGAAGGG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC096362 282019 bp DNA linear HTG 10-M
Rattus norvegicus clone CH230-53N24, WORKING DRAFT SEQUENCE.
AC096362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 58.9%; Pred. No. 4.1;
Matches 63; Conservative 0; Mismatches 44; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14384 TAGAGCATTAGATGGCTGTTTTTCTGAATGACAAGGAGTTCAGCTT 14430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 TAGTTAGTGATACACCGGTTATATCGGAGTGGCGAGAAAGTGTGGTT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
'organism="Rattus norvegicus"
'mol_type="genomic DNA"
'db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                              complement (235727, .236614)
                                                                                                                             1. 1575
/note="wgs end extension clone end:Sp6"
/note="clone boundary clone_end:Sp6
                                                                                                                                                                                                                                                                                                                                                                              end_sequence:BH305681"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   end_sequence:BH305680"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="clone_boundary
                                                                                                    clone="CH230-85M5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC096362.6 GI:30521829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone end:T7
                                                                                                                                                                                                                                                                                                                                              site: EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                site: EcoRI
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                                                                                                                                    misc_feature
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ORGANISM
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KEYWORDS
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Our Fourectulat and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA, On May 10, 2003 this sequence version replaced gi:22771585. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, hydidal sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature
                     Morgan, M. Morris, K. Morris, S. Munidasa, M., Munidasa, M., Morris, S., Mordelmeh, O., Okwuonu, G., Olarnpunsagonn, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Ploxofer, M., Rachin, E., Reeves, K., Redier, M.A., Reigh, R., Reilly, B., Rachling, E., Revers, K., Redier, M.A., Reigh, R., Sanders, M., Rachin, Y., Reuter, M., Rose, R., Ruiz, S. J., Sheuty, J., Sandery, T., Roiss, M., Rose, M., Rose, R., Ruiz, S. J., Shetty, J., Shartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C. Taylor, T., Thomas, N., Thomas, J., Mandron, L., Walker, B., Wang, J., Walght, M., Warren, J., Warken, K., Walker, B., Wang, J., Walght, D., Walght, R., Wallson, R., Walczyk, R., Wooden, H., Worley, K., Wilsh, D., Walch, J., Yoon, U., Yoon, U., Yau, S., Smith, H.O., Weinstock, G. and Gibbs, R.A., Smith, D.R., Smith, R.A., Smith, H.O., Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
2 (bases 1 to 282019)
Worldy,K.C.

Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 282019)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of I contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between the mare based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consensus quality: 236414 bases at least Q40 Consensus quality: 23934 bases at least Q30 Consensus quality: 2424934 bases at least Q30 Estimated insert size: 24249348, sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: Atlas 3.0;
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REFERENCE
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This sequence will be replaced

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ADVONCIOTINGO CONTROLL DITATER TERVERETVOLRORVAQAPERM ADVONCIOTINGO CONTROLLATION CONTROLLATION CONTROLLATION CONTROLLATION CONTROLLATION CONTROLLOR ROATAALMALSDVOND DERRETTSALLER TERVEGEER VACULO CONTROLLOR ROATAALMALSO CONTROLLOR ADVONCIOLORA CONTLORA CONTROLLOR LORDO CONTROLLOR ADVONCIOLORA CONTROLLOR RESEGNIVA CONTROLLOR RESEGNIVA CONTROLLOR RESEGNIVA CONTROLLOR RESEGNIVA CONTROLLOR CONTROLOR CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTRO
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/protein id="AAL1943.1"
/db xref="G1:16418987"
/translation="MERLPTPHDAVFRQMLMQKEVARDFLAIHMPEDFLAICDLDSL
KLEGGSFVEDNILRSEYSDILYSLHTCHGFGYYYALIEHQSKSDRLMAFRLMRYAIAAM
QRHLDAGHDTLDLVVPILFYHGPESPWPYSLNWHNMFVKFDMAKALYSRDFALVDLTT
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GNAAEPGALIROLAQGAPQYKEQLMTIAEWLEEKGRTEGLOKGLOKGLEQGLAQGREA
EARAIARKMLANGLEPGLIASVTGITPEELSTLSH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WALIRNLPGILEVLVISRLNMRQGASYAITTILNYVIIAVGAMTVFGSLGVSWDKLQW
LAAALSVGGFELQETGORPVSGLILIPERPVRIGDTVTGTGYSGTVSKTRIRATTT
DEDRKEVIIPNKAFVRERLIMWSLSDTTTRLVIRLGYKYGSDLEKVKRVLLQBAMEHP
KVMHDDEPAVFFTTGGASTLDHELRLYVREIRDRSHTVDELNRAIDRLCRENDINIAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="G1:16418986"
/translation="MTMLQLYKRSQHFVF1T1SVL11LLSCQSLAFARGQTNGDLPSK
                                                                                                                                         This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one mil subclone.

Location/Qualifiers
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/note="putative RBS for STM0479; RegulonDB:STMS1H000821"
were kindly provided by Heladia Salgado, Julio Collado-Vides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="similar to B. coli putative alpha helix protein (AAC73567.1); Blastp hit to AAC73567.1 (1120 aa), 89% identity in aa 1 - 1117"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="putative small-conductance mechanosensitive"
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/gene="STM0479"
/note="similar to B. coli orf, hypothetical protein
(AAC75365.1); Blastp hit to AAC75365.1 (296 aa), 49%
identity in aa 7 - 296"
                                               ReguonDB;
http://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset
                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Salmonella typhimurium LT2"
/mol_type="genomic DNA"
/strain="LT12", 6SSC 1412; ATCC 700720"
/db_xref="ATCC,700720"
/db_xref="taxon:99287"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'protein_id="AAL19432.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="synonym: STM0478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (4430. .4435)
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/transl_table=11
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/transl_table=:
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/gene="aefA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McClelland, M., Sanderson, K.E., Spieth, J., Clifton, S.W.,
Latreille, P., Courtney, L., Porwollik, S., Ali, J., Dante, M., Du, F.,
Hou, S., Layman, D., Leonard, S., Nguyen, C., Scott, K., Holmes, A.,
Grewal, N., Mulvaney, E., Ryan, E., Sum, H., Florea, L., Miller, W.,
Stoneking, T., Nhan, M., Waterston, R. and Wilson, R.K.
Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCT 23-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The analyses of ribosome binding sites and promoter binding sites
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Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs, GLIMMER; http://www.tigg.csg/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg/and Pedro Romero and Peter Karp at EcoCyc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (29-WAR-2001) Genome Sequencing Center, Department of Genetics, Washington University School of Medicine, 4444 Forest Park Boulevard, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Salmonella typhimurium LT2, section 26 of 220 of the complete
       by the finished sequence as soon as it is available and the accession number will be preserved.

1 282019: contig of 282019 bp in length.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 282019;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 TAGTTAGTGATACACCGGTTATATCGGAGTGGCGAGAAAGTGTGGTT
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                                                                                                                                                                                                /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-53N24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
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/note="wgs contig"
279586..280897
/note="wgs contig"
280948...282019
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Matches 63; Conserv
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MEDLINE
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KEYWORDS
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                                                                                                                             FEATURES
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Bitten, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Basten, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collywore, A., Cook, A., Cook, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Govette, M., Gage, D., Galagan, J., Gardyna, S., Gonde, S., Govette, M., Gage, D., Galagan, J., Gardyna, S., Gonde, S., Govette, M., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., Macdend, P., McKernan, K., Marguis, N., Matthews, C., Macden, C., Madonad, P., McKernan, K., Marguis, N., Matthews, C., Macden, C., Macden, C., Marguis, N., Marguis, N., Maldrim, J., Morban, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Salos, R., Schuuback, R., Stauss, N., Subramanian, A., Santos, R., Stongov, P., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strawers, M., Travers, M., Travis, N., Travi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18726 GGTAAAACACATGCCGACAGGGAGCGAGCACGGCATGGGATACTTATCCGTCCAGTAGCC 18785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18666 CGCAGCGAGCAATACGCCGCCAAACTTCCCGCCATTGCCAGCAGTACCAGCCCGCTCAG 18725
                                                                                                                   /EC number="2.7.7.7"
/BC number="2.7.7.7"
/note="DNA elongation factor III; DNA polymerase III
subunit TAU [contains: DNA polymerase III subunit gamma].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC099723 178993 bp DNA linear HTG 19-OCT-2002 Mus musculus clone RP23-369P21, WORKING DRAFT SEQUENCE, 8 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 GATAAAACCCACGTCGATAGCCCTCGACCGTCGCGTAATATTCTTAGAAAGCAAACAGCT
                                                                                                                                                                                                                                                                                                                tau and gamma subunits"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 CGCAGCAGCACGTCGTCGTCGTCATCGCCAACGGGAGTCGTGTTTTCGGTTCGATACA
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HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72;
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                             III,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 AAAGAACTATTTCAAGAACTGTGGGCAAG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                  /codon_start=1
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/product="DNA polymerase I:
/protein_id="AAL19438_1"
/db_xref="G1:16418992"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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                                        note="synonym: STM0484"
471. .8399
gene="dnaX"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34.8;
Pred. No. 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 178993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                14.6%;
52.0%;
               gene="dnaX"
                                                                                                                                                                                             subunit TAU
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 52.v.
78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                        /translation="MSLENAPDEVKLAVDLIVLLEENRLPARTVLRALEIVMRDYENK
LKSTEDDSQTE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="MLICTLERLATLRQRCAPLAQHATLSARFDRHLFRTRSTLLQG
YLEBACANLVALRQRVCHEQLPQVAMLAEHLASQLEAISRETAAMSLRQWDAAPGLG
RWQRRRIQHQEFERRLLAMTQERKIRLAQATGLVEQQTLQKEVEIYEGRLARCRHALE
KIENVLARLTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/trans__table=11
/product="putative phage gene 58"
/product="putative phage gene 58"
/prodein_id="AAL19436.1"
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RFHAMLLYRSWFGGYKRHWORYRAMPPGAKPRAIALILLTFGISLWLVNMWWVRVLLL
VILACLLIFWMRIPVIDEKQQKR."
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IELUVERYKNAGITKVVGTERRGFLFGAPVALGLGVGFVPVRKPRKLPRETTAETYEL
EYGTDQLEIHVDAIRFGDNVLVVDDLLATGGTIEATVKLIRRLGGKVTDAAFIINLFD
LGGEQRLEKGQITCYSLVPFPGH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to E. coli primosomal replication protein N'' (AAC73569.1); Blastp hit to AAC73569.1 (175 aa), 73% identity in aa 5 - 175"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to E. coli putative gene 58 (AAC73570.1);
Blastp hit to AAC73570.1 (125 aa), 84% identity in aa 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="putative RBS for ybam; RegulonDB:STMS1H000822"
complement(4680. .5195)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     t
t
                                                                                                                                              note="similar to E. coli orf, hypothetical protein (AAC73568.1); Blastp hit to AAC73568.1 (53 aa), 80%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="putative RBS for apt; RegulonDB:STMS1H000823"
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horte="similar to E. coli adenine
phosphoribosyltransferase (AAC73571.1); Blastp hit
AAC73571.1 (183 aa), 95% identity in aa 1 - 183"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="adenine phosphoribosyltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transI_table=11
fproduct="ynauthong replication protein N"
fprotein id="wh19455.1"
db_xref="GI:16418989"
                                                                                                                                                                                                                                                              'transT_table=11
|product="putative inner membrane protein"
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|db_xref="GI:16418988"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="synonym: STM0481"
complement (4680. .5195)
                                                           'note="synonym: STM0480"
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/db_xref="GI:16418991"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5276. .5653
/gene="yban"
/note="synonym: STM0482"
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complement (4499. .4677)
                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (4672. .4677)
/gene="ybam"
                                                                                          complement (4499. .4666)
                                                                                                                                                                                                          dentity in aa 1 - 49"
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/transl_table=11
                                                                                                                                                                                                                                      start=1
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transI table=
                                                                                                                      'dene="ybaM"
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/gene="yban"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="priC
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/gene="apt"
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|gene="apt"
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AC113984
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            Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chaspal, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Farco, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Grand-Pierre, N., Hafez, N., Hafez, N., Hades, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Landers, T., Levine, R., Liu, G., Machean, C., Macdonald, P., Major, J., Mathews, C., McCarthy, M., Meldim, J., Meneus, L., Mihova, T., Machean, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vossillev, H., Viel, R., Wilson, B., Wu, X., Travers, M., Vossillev, H., Viel, R., Volon, B., Wilson, B., Wwan, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (19-OCT-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Oct 19, 2002 this sequence version replaced gi:16974222.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research
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Conter clone name: 369 P.21

Sequenching vector: plasmad; n/a; 100% of reads
Sequenching vector: plasmad; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 17482 bases at least Q30

Consensus quality: 17784 bases at least Q20

Insert size: 183000; agarose-fp

Insert size: 178293; sum-of-contigs

Quality coverage: 10.8 in Q20 bases; samo-of-contigs

Quality coverage: 11.1 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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9858: contig of 1085 bp in length
9958: gap of 100 bp
19220: contig of 9262 bp in length
19320: gap of 100 bp
29525: contig of 10205 bp in length
29625: gap of 100 bp
95507: contig of 65882 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
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8 128597: contig of 32990 bp in length
8 128697: contig of 43628 bp in length
8 172325: contig of 43628 bp in length
6 173493: contig of 6568 bp in length.
10cation/Qualifiers
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(bases 1 to 178993)
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19221
19321
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95508
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128598
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172426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
REFERENCE
                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
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Ongolished

Dipublished

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115622 ATAGTTCTTTTAAAATATGTATTTCAATTATGTGGTGAGGAGGACTGCAAATGTCCTA 115563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC113984 193636 bp DNA linear HTG 21-0CT-2002 Mus musculus clone RP24-97D3, WORKING DRAFT SEQUENCE, 13 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 193636)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 GATAAAACCCACGTCGATAGCCCTCGACCGTCGCGTAATATTCTTAGAAAGCAAACAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115682 GCTTAACCACAGGCCATCTCCCCAGGCCTCCTGGAAGTAACTTTTAAACCACTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                              clone_lib="RPCI-23 Female Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115562 GAAGCTAGAAGAGGATGTGACCCCGGGGCTGGTC 115529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACI13984
ACI13984.3 GI:24182209
HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 TCGGAGTGGCGAGAAGTGTGGTTCCGGCTGGAC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP24-97D3
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Best Local Similarity 51.33
Matches 79; Conservative
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3256 GGCCAGGGGGCTGTGGATTTCCTTTAGTTTCAGAGCACTCAGACTGCCAAATCCCTGTA 3315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 CCGTCGCGTAATATTCTTAGAAAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGTGGC
                            contig of 4924 bp in length gap of 100 bp contig of 48775 bp in length contig of 48775 bp in length gap of 100 bp contig of 3843 bp in length contig of 7892 bp in length gap of 100 bp contig of 23083 bp in length contig of 23083 bp in length gap of 100 bp contig of 36507 bp in length gap of 100 bp contig of 24277 bp in length gap of 100 bp contig of 34277 bp in length contig of 31067 bp in length gap of 100 bp contig of 31067 bp in length gap of 100 bp contig of 31067 bp in length gap of 100 bp contig of 31067 bp in length gap of 100 bp contig of 31067 bp in length
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Best Local Similarity 54.5%; Pred. No. 43;
Matches 67; Conservative 0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .1188
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1289. .3601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="assembly_fragment"
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vector_side:right"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .66508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66609. .74500
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66608:
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74600:
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8767
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158768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
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Barran, B., Nusbamu, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barren, B., Nusbamu, C., Lander, E., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gard, S., Graham, L., Grand-Pierre, N., Hafez, N., Horton, L., Hulme, M., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Mathews, C., Nccarthy, M., Meldrim, J., Meney, L., Mihova, T., Mathews, C., Nccarthy, M., Weldrim, J., Meney, E., Mihova, T., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Travers, M., Vossiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., M., Dirtted (21-007-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA
On Oct 21, 2002 this sequence version replaced gi:21327615.
Smit, A.F.A. & Green, P. (1996-1997)
http://ftb.genome.washington.edu/RM/RepeatMasker.html
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Sturge-Thomann, N., Stolupback, R., Seaman, S., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tollama, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Voil, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                               Submitted (06-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 193636)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 1188 contig of 1188 bp in length

* 1289 3601: contig of 2313 bp in length

* 3702 6708: contig of 3007 bp in length

* 6709 6808: gap of 100 bp

* 6808: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L24343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center clone name: 97
                                                                                                                                                                                                TITLE
JOURNAL
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JOURNAL
                                                                                                                                                                                                                                                                        REFERENCE
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COMMENT

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Gaps 0;

Length 193636;

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* NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 12781 12880; contig of 12780 bp in length

* 12781 13370; contig of 490 bp in length

* 13471 14758; contig of 1288 bp in length

* 14759 14858; gap of 100 bp
                                                        Contact: sequence submissions@genome.wi.mit.edu
------- Project Information
Center project name: L22358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160943: gap of 100 bp
216116: contigg of 55173 bp in length
216216: gap of 100 bp
229102: contig of 12886 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of 22068 bp in length gap of 100 bp contig of 40435 bp in length
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of 14093 bp in length
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of 56421 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig of 3105 bp in length
gap of 100 bp
contig of 2813 bp in length
gap of 100 bp
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of 6450 bp in length
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14859. 17963
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                                                                                                                                                                                                                                                                                          Direct Submission

Submitted (0.2-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Search, 320 Charles Street, Cambridge, MA 02141, USA

Si (bases 1 to 229102)

Si baren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Cook, A., Cook, D., Corum, B., Charellan, V., Cook, P., Cook, D., Corum, B., Charellan, V., Farco, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, M., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kells, M., Mabbitt, R., Maclean, C., Macoland, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Maldrim, J., Meneus, L., Mihow, T., Manday, V., Marghy, T., Naylor, J., O'Neil, D., Oliver, J., Peterson, K., Flunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Stebe, C., Rogov, P., Rochupka, A., Ramasamy, U., Raymond, C., Retta, R., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Warett, Submission
                        AC119849 229102 bp DNA linear HTG 22-FEB-2003
Mus musculus clone RP23-7404, WORKING DRAFT SEQUENCE, 12 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
Submitted (22-FEB-203) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 22, 2003 this sequence version replaced gi:20389488.
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                 AC119849.2 GI:28467231
HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                         Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-7404
                                                                                                                                                                                                                         (bases 1 to 229102)
                                                                                                                                                                                                                                                                               Unpublished
                                                                                     AC119849
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JOURNAL
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TITLE
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JOURNAL
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                                                                                   ACCESSION
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                                                                                                       VERSION
KEYWORDS
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                                                                                                                                                                                                                         REFERENCE
          AC119849
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COMMENT

misc_feature

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122376 GGCCAGGGGGCTGTGGATTTCCTTTAGTTTCAGAGCACTCAGACTGCCAAATCCCTGTA 122435
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                                                                                                                                                                                                                                                                                                      110 CCGTCGCGTAATATTCTTAGAAAGCAACTAAAAGAACTATTTCAAGAACTGTGGG 169
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Best Local Similarity 54.5%; Pred. No. 44;
Matches 67; Conservative 0; Mismatches 56; Indels 0; Gaps
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                  Copyright
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OM nucleic - nucleic search, using sw model

September 18, 2004, 09:40:06; Search time 257.309 Seconds (without alignments) 3945.922 Million cell updates/sec Run on:

US-10-614-282-1 239

1 atcagtcacgacttggtaag.........tgtggttccggctggacaat 239 Title: Perfect score: Sequence:

IDENTITY NUC Scoring table:

residues 3373863 seqs, 2124099041 Gapop 10.0 , Gapext 1.0 Searched:

6747726 of hits satisfying chosen parameters: Total number

length: 0 length: 2000000000 DB sed DB sed Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_29Jan04:* Database

geneseqn1980s:* geneseqn1990s:* geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002s:* geneseqn2003as:* geneseqn2003bs:* geneseqn2003cs:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:*

SUMMARIES

Description	Abl02306 Drosophil		Adbe8937 C. neofor	Aba01441 Streptoco		Continuation (23 o	Abl04264 Drosophil	Abq30441 Oliqonucl		Aas45335 Chemicall	Aaq60282 Human bra	Abl20185 Drosophil		Continuation (5 of	Continuation (3 of	Abs55200 Genomic D	Aba21393 Human ner	Aba21394 Human ner	Ada71938 Rice gene		Abl67239 Thyroid c		Abq70841 Listeria
a l	ABL02306	ABQ70202	ADB68937	ABA01441	ACA36437	ABA03041 22	ABL04264	ABQ30441	ABQ30440	AAS45335	AAQ60282	ABL20185	ABL14353	ABS55320 4	ABS55320 2	ABS55200	ABA21393	ABA21394	ADA71938	ABL64403	ABL67239	ABQ68462	ABQ70841
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% Query Match	100.0	13.7	13.4	13.3	13.2	13.2	13.1	13.0	13.0	13.0	12.9	12.9	12.9	12.9	12.9	12.9	12.6	12.6	12.6	12.6	12.6	12.6	12.6
Score	239	32.8	32	31.8	31.6	31.6	31.2	31	31	31	30.8	30.8	30.8	30.8	30.8	30.8	30.2	30.2	30.2	30.2	30.2	30	30
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Aba20697 Human ner	Aah41224 Pyrococcu	Acf73872 Staphyloc	Aag73396 CviJI ORF	Aav74866 Staphyloc	Aaq73395 CviJI cod	Continuation (22 o	Aaa70287 Plasmodiu	Acc80906 Human CYP	Aac35767 Zea mays	Abk35684 cDNA segu	Aas72544 DNA encod	Abx46645 Bovine ES	Abv15324 Human pro	Aca23730 Prokaryot	Aca30362 Prokaryot	Aca52220 Prokaryot	Adc86940 Human GPC	Adc87621 Human GPC	Aas37706 Novel hum	Aah52955 S. epider	Abz51987 Aspergill
ABA20697	AAH41224	ACF73872	AAQ73396	AAV74866	AAQ73395	ABA03041 21	AAA70287	ACC80906	AAC35767	ABK35684	AAS72544	ABX46645	ABV15324	ACA23730	ACA30362	ACA52220	ADC86940	ADC87621	AAS37706	AAH52955	ABZ51987
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29.8	29.8	29.6	29.6	29.6	29.6	29.6	29.4	29.4	29.5	29.5	29.5	59	29	29	28.8	28.8	28.8	28.8	28.6	28.6	28.6
24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

developmental biology; cell signalling; insecticide; Drosophila melanogaster expressed polynucleotide SEQ ID NO 1400. ABL02306 standard; cDNA; 18920 BP. 23-MAR-2001; 2001WO-US009231. (first entry) Drosophila; developmental pharmaceutical; gene; ss Drosophila melanogaster. WO200171042-A2. 26-MAR-2002 27-SEP-2001 ABL02306; RESULT 1 ABL02306

23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150. (PEKE) PE CORP NY

Myers EW; Li PWD, Adams M, Venter JC,

WPI; 2001-656860/75 P-PSDB; ABB58203 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

Claim 1; SEQ ID NO 1400; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL3611), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly

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Gaps

0;

27; Indels

Length 727;

Matches

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The invention relates to a novel purified or isolated Cryptococcus neoformans nucleic acid molecule comprising a sequence encoding a polypeptide comprising a sequence not given in the specification. A polynucleotide of the invention has fungicide activity, and may have a use in gene therapy. The nucleic acid is useful for preparing a composition for treating an infection caused by Cryptococcus neoformans. The present sequence represents a C. neoformans sequence of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.
                                                                                                                                                                                     88 AACCCACGTCGATAGCCCTCGACCGTCGCGTAATATTCTTAGAAAGCAAACAGCTAAAGA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 TTTTCGGTTCGATACAGATAAACCCACGTCGATAGCCCTCGACCGTCGCGTAATATTCT 126
                                                                                                                                                                                                                                214 AACCAAAATTGATAGGCCTCGTCCGTATCGTATAATTCCTTCACGAAAAAGTAAACTA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 CACGACTTGGTAAGCGCGCAGGCAGGCACGTCGTCGTCGTCGTCATCGCCAACGGGAGTCGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395 CAGGGCATCGGCATCCCCCTCACAGCAGATCTACGTCCTAACCGCCGACGGTTCACGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid, useful for preparing a composition for treating infection caused by Cryptococcus neoformans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.4%; Score 32; DB 9; Length 3250; 52.2%; Pred. No. 3.3;
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                                                Sequence 727 BP; 225 A; 106 C; 164 G; 231 T; 0 U; 1 Other;
                                                                                         13.7%; Score 32.8; DB 6; 64.5%; Pred. No. 0.92; iive 0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C. neoformans genomic DNA sequence SEQ ID NO:64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ds; gene; fungicide; gene therapy; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
  on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; SEQ ID NO 64; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB68937 standard; DNA; 3250 BP
                                                                                                                                                                                                                                                                                                                            154 GACAAAACAAGATCTG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-2002; 2002WO-US040225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-DEC-2001; 2001US-0341261P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                148 ACTATTTCAAGAACTG
                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zamudio C, Eroshkin AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cryptococcus neoformans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2003-533017/50.
                                                                                                               Local Similarity
nes 49; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB68937;
                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
ADB68937/c
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                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                        941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              762 ATCAGTCACGACTTGGTAAGCGCGCAGGCAGCACGTCGTCGTCGTCATCGCCAACGGGAG 821
                                                                                                                                                                                                                                                                                                                121 TATTCTTAGAAAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGGGCAAGTGAAGGGT 180
                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                   TCGTGTTTTTCGGTTCGATACAGATAAAACCCACGTCGATAGCCCTCGACCGTCGCGTAA
                                                                                                                                                                                       1 ATCAGTCACGACTTGGTAAGCGCGCAGCAGCACGTCGTCGTCGTCATCGCCAACGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                     882 TATTCTTAGAAAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGTGGCAAGTGAAGGGT
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTTAGTGATACACCGGTTATATCGGAGTGGCGAGAAAGTGTGGTTCCGGCTGGACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibacterial; Listeria; food contamination; mutational analysis; infection; ds.
                                                Sequence 18920 BP; 5734 A; 4166 C; 3925 G; 5095 T; 0 U; 0 Other;
                                                                                                                                         .,
                                                                                                Length 18920;
                                                                                           100.0%; Score 239; DB 4; Length 1
100.0%; Pred. No. 2e-71;
ive 0; Mismatches 0; Indels
from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Listeria monocytogenes 4b contig DNA sequence #144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; SEQ ID NO 3015; 180pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listeria monocytogenes ATCC 19115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
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                                                                                                                                            Conservative
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CENT NAT
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                                                                                                                   Local Similarity
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(CNRS ) CNRS
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29-AUG-2002
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                                                                                                                                         239;
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                                                                                                Query Match
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ABQ70202/c
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92 ;

us-10-614-282-1.rng

Antisense; ds; prokaryotic essential gene; cell proliferation;

Listeria monocytogenes

WO200277183-A2.

drug design; gene

Prokaryotic essential gene #18094

19-JUN-2003 (first entry)

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ö
335 CTTCCTCCATCCTACAAGACGGAAGGAAGAACTCCACCATACGCATCTTTCCC 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 TAAAACCCACGTCGATAGCCCTCGACCGTCGCGTAATATTCTTAGAAAGCAAACAGCTAA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid fragments containing exopolysaccharide operon, useful e.g. for increasing exopolysacchride synthesis in lactic acid bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Exopolysaccharide; lactic acid bacterium; eps; fermented food product;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus thermophilus eps3 operon #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INRG ) INRA INST NAT RECH AGRONOMIQUE
(DANO-) CIE DANONE SA GERVAIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Page 75-80; 144pp; French.
                                                                                                                                                                                                                                                                                                                                                                          ABA01441 standard; DNA; 17468 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                             TAGAAAGCAAACAGCT
                                                                                                                                                                                       TATACAACATATCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-017616/02.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                          HANDER STANDER STANDER
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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

Zamudio C, Trawick JD, 2003-029926/02

'n, Wang Wall WPI: P-PSDB; ABU32567

; 2001US-00815242. ; 2001US-00948993. ; 2001US-0342923P. ; 2002US-00072851.

2002US-0362699P

25-OCT-2001; 08-FEB-2002; 06-MAR-2002;

(ELIT-) ELITRA PHARM INC.

2002WO-US009107

21-MAR-2002; 21-MAR-2001; 06-SEP-2001;

03-OCT-2002

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the inversion retained by the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated of polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of which each of the strains is present in a culture or collection of confound that inhibits the capiliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation of an organism. The antisense modeled acids are useful for drug discovery programs, or for screening homologous nucleic acids required for cellular proliferation of an organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               this patent did
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence is one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K. pneumoniae or P. aeruginosa. The present sequence is one o
prokaryotic essential genes. Note: The sequence data for this
not form part of the printed specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 969;
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Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14;
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TAAAAACCACGACAATAGTCTTCAACAATATCTTGATATCCGACCAAATCGACCAGTTAT 7568

7627

g à g

7567 CGATATATTCAACATCGAGTCTTACCACCTCATCAAAGTTGGTAATA 7521

ACA36437 standard; DNA; 969

ACA36437;

RESULT 5
ACA36437
ID ACA3
XX
AC ACA3

WO200171042-A2

108 GACCGTCGCGTAATATTCTTAGAAAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGTG 167

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9530 GATAATTTCAAATTACTGCATGCCCATTGAATGTGATTCAATTAGAGACTCCTGTTTTC 9589
                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9470 TCACACACACATGGCTTTCCACCTCAAGCCCTATTCTAATGAAATATAGCAATTACCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 TAAAACCCACGICGATAGCCCTCGACCGTCGCGTAATATTCTTAGAAAGCAAACAGCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytosine methylation; S'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide for detecting cytosine methylation SEQ ID NO 17032
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11638 BP; 3301 A; 2602 C; 2428 G; 3307 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
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13.1%; Score 31.2; DB 4; Length 11638;
Best Local Similarity 51.4%; Pred. No. 11;
Matches 72; Conservative 0; Mismatches 68; Indels 0;
                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 7274; 21pp + Sequence Listing; English.
                                                                                                                                    Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9590 CCAAGCAAGACAAAAGGIGG 9609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 GGAGTGGCGAGAAAGTGTGG
                                                                                                                                    PWD,
                                                                       23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                 23-MAR-2001; 2001WO-US009231.
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                                                                                                                                    Venter JC, Adams M,
                                                                                                                                                             WPI; 2001-656860/75.
                                                                                                            PEKE ) PE CORP NY
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                        27-SEP-2001
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                                                                                                                                   of 30) of ABA03041 from base 2200001 (iisteria monocytogenes EGD-e gend into 30 fragments LOCUS ABA03041 Accession Aba03041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 GACCGTCGCGTAATATTCTTAGAAAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGTG 167
                     7 GAACAAAGAAAAATTATTAGAAATTCATAATCTAAAGCAATACTTTAACAAAGGTACT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster expressed polynucleotide SEQ ID NO 7274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 110000;
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Pred. No. 20;
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Conservative
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2800001
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                                                 168 GCAAGTGAAG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAAGTGAAG 177
                                                                        67 GCAAGTGAAG
                                                                                                                                      Continuation (23 of 30)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                 Sequence split in
Fragment Name
                                                                                                                                                                       ABAÓ3041_00
ABAO3041_01
ABAO3041_02
ABAO3041_03
ABAO3041_04
ABAO3041_06
ABAO3041_06
ABAO3041_07
ABAO3041_07
ABAO3041_09
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ABA03041_18
ABA03041_19
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ABA03041 11
ABA03041 12
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ABA03041_14
ABA03041_15
ABA03041_16
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ABA03041_21
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ABA03041 26
ABA03041 27
ABA03041 28
ABA03041 29
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ABA03041_24
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144

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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonacleotides and/or peptide-nucleic acid (PNA) oligoners and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of clip amplicon. From the ratio of labels hybridised to the two classes of oligoners, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the methylation status of many C residues to be determined simultaneously, ABQ13410.
                                                                                                                                                                                                                                                                   Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ54121 represent genomic DNA sequences used to illustrate the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for determining the degree of cytosine methylation described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 536 BP; 189 A; 188 C; 65 G; 94 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                               Claim 12; 56pp + Sequence Listing; 56pp; German
                                                                                                                                                                          Guetig D;
                                                                                                                                                                       Berlin K,
  01-SEP-2001; 2001WO-EP010074.
                                        01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                            diagnosis and prognosis, cor
from chemically treated DNA
                                                                                                                                                                       Piepenbrock C,
                                                                                                                     (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                     WPI; 2002-371829/40.
                                                                                                                                                                  olek A,
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (BNA) oligomers and the degree of hybridisation to both classes is determined from the label on the ratio. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method is considered the invention.

Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons

losis and prognosis, conchemically treated DNA.

Guetig D;

Berlin K,

Piepenbrock C,

olek A,

WPI; 2002-371829/40.

(EPIG-) EPIGENOMICS AG.

01-SEP-2001; 2001WO-EP010074 01-SEP-2000; 2000DE-01043826

2000DE-01044543

05-SEP-2000;

Claim 12; 56pp + Sequence Listing; 56pp; German.

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                                                                                       CGTCGTCGCCGCCATCCTCGACGCGACTCGCTTTTCGATTCTACCTAAAAAATCCAC 252
                                                                34 CGTCGTCGTCGTCATCGCCAACGGGAGTCGTGTTTTTCGGTTCGATACACATAAAACCCA 93
                                          Gaps
                                          .,
            Score 31; DB 6; Length 536;
Pred. No. 3.4;
0; Mismatches 25; Indels
             13.0%;
64.8%;
Query Match
Best Local Similarity 64.84
Best Local 46; Conservative
                                                                                                                    CGTCGATAGCC 104
                                                                                                                                            CGCCATCCGCC 263
                                                                                         193
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94 CGTCGATAGCC 104 decenteded 274

34 CGTCGTCGTCGTCATCGCCAACGGGAGTCGTGTTTTTCGGTTCGATACAGATAAAACCCA

6

Gaps .,

Length 536; 25; Indels

Sequence 536 BP; 94 A; 65 C; 188 G; 189 T; 0 U; 0 Other;

disclosure of the invention

13.0%; Score 31; DB 6; larity 64.8%; Pred. No. 3.4; Conservative 0; Mismatches 25

Query Match Best Local Similarity Matches 46; Conservat

à 셤 à g

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Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                 Oligonucleotide for detecting cytosine methylation SEQ ID NO 17031.
                        BP
                       ABQ30440 standard; DNA; 536
                                                                         (first entry)
                                                                        12-JUL-2002
                                                ABQ30440;
         RESULT 9
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WO200218632-A2 Homo sapiens

07-MAR-2002

Cell cycle, human, CpG dinucleotide, cytosine methylation, HIV; aging, human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease, Lewy body disease, cancer; arthritis; arteriosclerosis; anti-HIV; neuropycotective; antiarthritic; immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds; Chemically pretreated complementary DNA associated with cell cycle #20. (first entry) Homo sapiens, 18-DEC-2001

AAS45335 standard; DNA; 6061 BP.

RESULT 10 AAS45335/c

AAS45335;

(EPIG-) olek A,

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The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTs which can be used as markers for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed genes on chromosomes, for individual or forensic identification, for mapping locations of disease-associated genes, for identification of tissue type, and for prepn. of antisense sequences, probes and constructs. EST02279 has a "poor" coding probability as evaluated using the coding-region prediction program CRM. See also AAQ59041-Q61440. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 GTAATATTCTTAGAAAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGTGGCAAGTGAA 176
                                                                                                                                                                                                                                                                                                                                                                                            Enriched oligonucleotides and corresp. sequences - used as markers for
human genes transcribed in-vivo, facilitate tagging of most human genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 GCAGCATCCTTACCTTGCAGAGTACTGAGTCCTGGCTTCATGAATTTNATGTCAAGTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
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Pred. No. 3.5;
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                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page 310; 500pp; English
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2000US-00614150
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                                                                                                                                                                                                                                                               Venter CJ, Adams MD,
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Best Local Similarity
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19-AUG-1993
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic analysing cytosine methylations in the pretreated of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, arthritis, solid tumours and cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene transcription product; genetic markers; tagging; in vivo; transcription; mapping; locations; chromosomes; chromosomal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31; DB 4; Length 6061;
Pred. No. 9.6;
0; Mismatches 25; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 40; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                             06-APR-2000; 2000DE-01019058.
07-APR-2000; 2000DE-01019173.
30-UNA-2000; 2000DE-01035529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                             15-MAR-2001; 2001WO-EP002945.
                                                                                                                                                                                                 .5-MAR-2000; 2000DE-01013847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.0%;
Best Local Similarity 64.8%;
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ60282 standard; DNA; 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              associated with cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2104 CGCCATCCGCC 2094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-602751/68
   WO200168911-A2
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                                                                                                                                                                                                                                                                                                                                                             73
                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therepeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                   611 İGGİACGIĞAĞCÇAĞTIÇĞİÇĞİÇİÇÇÇĞÇÜĞİTĞGAAİTÜTTÇAĞÇAAĞĞİTĞIĞĞĞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                        14 TGGTAAGCGCGCAGCACGTCGTCGTCGTCATCGCCAACGGGAGTCGTGTTTTTCGG
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster expressed polynucleotide SEQ ID NO 37541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                          Score 30.8; DB 4; Length 1625; Pred. No. 6.4;
                                                                                                                                                                                                                                                         Sequence 1625 BP; 410 A; 413 C; 387 G; 415 T; 0 U; 0 Other;
                                                   English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ID NO 37541; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                           37; Indels
                                                NO 12028; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                671 ATGITITGAATAAACCCCGCGTCTATAAC 700
                                                                                                                                                                                                                                                                                                                                                                                                                      74 TTCGATACAGATAAAACCCACGTCGATAGC 103
                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EW;
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                                                                                                                                                                                                                                                                                          12.9%;
58.9%;
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2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                       Query Match 12.9
Best Local Similarity 58.9
Matches 53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
from Drosophila
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                                              Claim 1; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; ABB70250
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                  interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEKE ) PE
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(Human transporter protein genomic DN Accession Abs55320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38069 TAAAAGAATCTCCTTTCACCTAAAATACTAACAACTGCATAAGCATTTTTAAT 38010
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                                                                                                                                                                                                  724 IGGIACGIGGICAGCIAGIICGICGICICCCCCGIIGGAAICIICAGCAAGGIIGIGCIG 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164
                                                                                                                                                                           73
           sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                      TGGTAAGCGCGCAGCAGCACGTCGTCGTCATCGCCAACGGGAGTCGTGTTTTTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCGACCGTCGCGTAATATTCTTAGAAAGCAAACAGCTAAAAGAACTATTTCAAGAACTGT
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 TCATCGCCAACGGGAGTCGTGTTTTCGGTTCGATACAGATAAAACCCACGTCGATAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 CTCGACCGTCGCGTAATATTCTTAGAAAGCAAACAGCTAAAAGAACTATTTCAAGAACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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    expressed DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6; Length 106286;
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0
                                                                                                                 Length 1738;
                                                                                 Sequence 1738 BP; 454 A; 440 C; 425 G; 419 T; 0 U; 0 Other;
                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
 discloses genomic DNA sequences (ABL16176-ABL30511),
                                                                                                                                          37;
                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72;
                                                                                                                                                                                                                                                                                                                             from base 400001
LOCUS ABS55320
End
                                                                                                                             Pred. No. 6.6;
0; Mismatches
                                                                                                                                                                                                                           74 TTCGATACAGATAAACCCCACGTCGATAGC 103
                                                                                                                                                                                                                                                       784 AIGTTITTGAATAACCCCCCCCCTTATAAC 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30.8; DI
Pred. No. 38;
0; Mismatches
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                                                                                                                Score 30.8;
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Pred. No. 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGGCAAGTGAAGGGTAGTTAGTGAT 190
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410000
506286
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                                                                                                                                                                                                                                                                                                                                             fragments
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                                                                                                                12.9%;
58.9%;
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larity 50.7%;
Conservative
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50.7%;
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300001
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300001
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                                                                                                              Query Match 12.9
Best Local Similarity 58.9
Matches 53, Conservative
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5
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Continuation (5 of 5) of
WP Sequence split into 5
WP Fragment Name
WP ABS53320-0
WP ABS53320-1
WP ABS53320-2
WP ABS55320-3
WP ABS55320-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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Continuation (3 of 5) or
WP Sequence split into
WP Fragment Name
WP ABS55320_0
WP ABS55320_1
WP ABS55320_3
WP ABS55320_3
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es 74; Conser
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Fragment Name
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ABS55320_2
ABS55320_3
ABS55320_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Sim
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Search completed: September 18, 2004, 11:29:54 Job time : 261.309 secs

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APPLICANT: Svaminathan, Neela
APPLICANT: Wan Etten, James
APPLICANT: Mead, David
APPLICANT: Mead, David
APPLICANT: Recompliant CviJI Restriction Endonuclease
TITLE OF INVENTION: Recombinant CviJI Restriction Endonuclease
CORRESPONDENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.4%; Score 29.6; DB 1; Length 1225; Best Local Similarity 64.7%; Pred. No. 1.1; Matches 44; Conservative 0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,629A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 6300 Sears Tower, 233 South CITY: Chicago STATE: 111inois COUNTRY: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: 1BM PC Compatible COMPUTER: 1BM PC Compatible COMPUTER: 1BM PC COMPATIBLE STSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08181629A; Patent No. 5472872; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, David W.
REGISTRATION NUMBER: 36.107
REFERENCE/DOCKET NUMBER: 3150
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPAK: 312/474-6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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EDNESS: single
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CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
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Sequence 118, App
Sequence 1118, App
Sequence 196, App
Sequence 746, App
Sequence 2060, App
Sequence 2060, App
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1397, Ap
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Seguence 4, Appli
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                                                                                                                                       September 18, 2004, 11:14:16; Search time 59.8737 Seconds (without alignments) 2215.217 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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. /cgn2_ 6/ptodata/2/ina/5A_COMB.seq:*
. /cgn2_ 6/ptodata/2/ina/5B_COMB.seq:*
. /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
. /cgn2_ 6/ptodata/2/ina/6B_COMB.seq:*
. /cgn2_ 6/ptodata/2/ina/PCTUS_COMB.seq:*
. /cgn2_ 6/ptodata/2/ina/PCTUS_COMB.seq:*
. /cgn2_ 6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-134-001C-1118
US-09-339-478-196
US-08-998-416-746
US-09-543-681A-2060
US-09-358-082A-3186
US-09-328-328-33
US-09-328-352-1397
US-09-358-082A-29
US-09-358-082A-29
US-09-621-976-15639
US-09-910-174B-3
US-09-910-174B-3
US-09-910-174B-3
US-09-910-174B-3
US-09-910-174B-1
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US-09-489-039A-4389
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Maximum Match 100%
Listing first 45 summaries
                                                                                              nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 2000000000
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Match Length DB
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Sequence	5-921-45 Sequence 45,	Seguence	4-918-37 Sequence 37	5-315-37 Sequence 37	5-315-37 Sequence 37	5-417-37 Sequence 37	8-709-37 Sequence 37	7-745-37 Sequence 37	US-08-956-171E-124 Sequence 124,	US-09-198-452A-1 Sequence 1	1-891-79 Sequence 79,		Sequence		Sequence	JS-09-641-638-620 Sequence 620,	JS-09-641-638-621 Sequence 621	MENTS
US-09-999-201B-3	US-09-566-921-45	US-09-790-988-1	US-08-714-918-3	US-09-265-315-37	US-09-265-315-37	US-09-266-417-37	US-09-528-709-37	US-09-527	US-08-956	US-09-19	US-08-781-891-79	US-09-618-166-79	US-09-791-211-3	US-09-641-638-42	US-09-641-638-43	US-09-641	US-09-641	ALIGNMENTS
4047 4	9610 4	640681 4	2515 3	2515 3	2515 3	2515 3	2515 4	2515 4	7762 4	1230025 4	87350 3	87350 4		956 4	956 4	1001 4	1001 4	
11.1	11.1	11.1	11.0	11.0	11.0	11.0	11.0	11.0	11.0	11.0	11.0	11.0	11.0	10.9	10.9	10.9	10.9	
26.6	26.6	26.6	26.4	26.4	26.4	26.4	26.4	26.4	26.4	26.4	26.2	26.2	26.2	26	26	26	26	
28	29	c 30	31	32	33	34	35	36	c 37	38	9	40	41	c 42	c 43	c 44	c 45	

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                                                                                                                                                                                                                                                                                                      Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
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1016 drarcdrererraritregiesaaararearreaceerareareereeraceera 957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.4%; Score 29.6; DB 4; 50.0%; Pred. No. 1.2; tive 0; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-0ct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: P5248P1
TELECONGUNIONINFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-6439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 TAGTTAGTGATACACCGGTTATATCGGA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 555:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                       RESULT 2

0.08-95-171E-555/c

Sequence 555, Application US/08956171E

Patent No. 6593114

GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1472 base pairs
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 50.0
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Maryland
                                                                                    191 ACACCGGT 198
                                                                                                                            751 GCACCGGT 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-956-171E-555
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Sequence 1118, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPBUTICS
FILE REPRESENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
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                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Swaminathan, Neela
APPLICANT: Swaminathan, James
APPLICANT: Wead, David
APPLICANT: Skowron, Piotr
TITLE OF INVENTION: Recombinant CviJI Restriction Endonuclease
NUMBER OF SECUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 5496;
                                                                                                                                                                                                                                                                                                                                                                                              3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: United States of America 2TP: G0606-6402 COMPUTER READABLE FORM: CMDUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: DATENT Helease #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/181,629A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
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12.4%; Score 29.6; DB 1;
Best Local Similarity 64.7%; Pred. No. 2.2;
Matches 44; Conservative 0; Mismatches 24;
896 TAATGCGTTATCATTCATTAATTGCTGA 869
                                                                                                                                                Sequence 2, Application US/08181629A Patent No. 5472872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36.107
REFRENCE/DOCKET NUMBER: 3150
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 5496 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1819 GCACCGGT 1826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                             1618 GARACACATCAAAGCGAAAAACAAAGCACACAAAGTCTCAACAAATAGATATTGCTCAA 1677
                                                                                                                                                                                                                                                                                                   77 GATACAGATAAAACCCACGTCGATAGCCCTCGACCGTCGCGTAATATTCTTAGAAAGCAA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 ATAGCCCTCGACCGTCGCGTAATATTCTTAGAAAGCAAACAGCTAAAGAACTATTTCAAG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Wohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                   Length 1731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 196, Application US/09397787

Sequence 196, Application US/09397787

GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Lodes, Michael J.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CVARIAN
TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS
FILE REFERENCE: 21012.466C2
CURRENT APPLICATION NUMBER: US/09/397,787
CURRENT APLICATION NUMBER: US/09/397,787

CURRENT FILING DATE: 1999-09-16

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 196

LENGTH: 423
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                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                               12.0%; Score 28.6; DF ilarity 59.0%; Pred. No. 2.9; Conservative 0; Mismatches
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Pred. No. 2.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 AACTGTGTGCCAAGTGAAGGGTAGTTA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 AGGAGGATAGGAAGGGGACAGTTGATA 152
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1118
LENGTH: 1731
                                                                                                                                                                                                                                                                                                                                                                                                                              1678 AAAGCTAAAGACTTATTTGGTGA 1700
                                                                                                                                                                                                                                                                                                                                                                                      137 ACAGCTAAAGAACTATTTCAAGA 159
                                                                                                                           TYPE: DNA
ORGANISM: Staphylococcus epidermidis
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Patent No. 6239264
GENERAL INFORMATION:
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ilarity 57.5%;
Conservative
                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapien
US-09-397-787-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                     US-09-134-001C-1118
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                        임
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GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543, 681A
CURRENT PAPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 454 GTACGAGCCGATGGTGAACGACTACGTGCTCAACGTGGACGAGAACTGTTTGATACAGTA 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 GTAAGCGCGCAGGCACGTCGTCGTCATCGCCAACGGGAGTCGTGTTTTTCGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27.6; DB 3; Length 716; Pred. No. 4.3; 0; Mismatches 44; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 CGATACAGATAAAACCCACGTCGATAGCCCTCGACCGT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             514 csáccraracaaaagccacricsacacacaarcscagr 551
                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 919-541-8587
TELEFRAX: 919-541-8689
              ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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; Sequence 2060, Application US/09543681A
; Patent No. 6605709
                                                                                                                                                                                                                                                                                                                        FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTONEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.5%;
nilarity 55.1%;
Conservative 0
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55.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 716 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 55.9
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 2060
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Best Local Similarity
Matches 54; Conserv
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APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1397
LENGTH: 1521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 CGGTTCGATACAGATAAAACCCACGTCGATAGCCCTCGACCGTCGCGTAATATTCTTAGA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 GCGTAATATTCTTAGAAAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGTGCGAAGTG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 cagciaaaiacagingcaaccacaingcaagingianacaingaaaigaggiciniga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 1200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 AAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGTGGGC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           422 AGTTAAATCCTTAAACCATGATTCAAACCATTGCTTAGC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
11.3%; Score 27; DB 4
Best Local Similarity 54.5%; Pred. No. 9.1;
Matches 54; Conservative 0; Mismatches
                                                                                                                                                                                 APPLICANT: Antoniou, Michael
APPLICANT: Crombie, Robert
TITLE OF INVENTION: A POLYMUCIECTICANT:
TITLE REFERENCE: CACOOOSE
CURRENT APPLICATION NUMBER: US/09/358,082A
CURRENT APPLICATION NUMBER: US/09/358,082A
CURRENT FILING DATE: 1998-07-21
PRIOR FILING DATE: 1998-07-21
PRIOR FILING DATE: 1998-07-21
PRIOR FILING DATE: 1998-07-21
PRIOR FILING DATE: 1998-07-21
PRIOR APPLICATION NUMBER: US 60/127410
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/127410
PRIOR PILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-23
PRIOR FILING DATE: 1999-04-23
PRIOR FILING DATE: 1999-04-23
PRIOR FILING DATE: 1999-05-12
PRIOR SED ID NOS: 29
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1397, Application US/09328352; Patent No. 6562958; GENERAL INFORMATION:
                                                                                            US-09-358-082A-27; Sequence 27, Application US/09358082A; Patent No. 6589784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acinetobacter baumannii
146 ATACCAAGATCTTTCAA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-328-352-1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-328-352-1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-358-082A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 27
LENGTH: 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           엄
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                                                                                                                                                                                                                               RESULT 8
US-09-107-532A-3186/C
; Sequence 3186, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; TILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES THERAPEUTICS
:- "monteNCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                     1235 TTGCTATGAGCGATAGACATAAAGCCTGCTTCAAAAGCCGACGGAGCGAGGTAATACGT 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 acercarparcarparcacaaaaresasarpsarasarcasarresarasarcasarrandas
                         TITITICGGITICGATACAGATAAAACCCACGTCGATAGCCCTTCGACCGTCGCGTAATATTC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 ACGICGICGICGICGICATCGCCAACGGGAGICGIGITITICGGIICGAIACAGAIAAAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31; Indels
                                                                                                                                                                    1175 rrrrcraacarraagregaagaacrerrraaag 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                        126 TTAGAAAGCAAACAGCTAAAGAACTATTTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1650
SEQUENCE DESCRIPTION: SEQ ID NO: 3186:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: PC
OPERATING SYSTEM: <Unknown:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 100 Beaver Street CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1650 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3186:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 ACGTCGATAGCCCTCGA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch
l Similarity 59.7%;
46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 46; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-107-532A-3186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 CGGTTCGATACAGATAAACCCACGTCGATAGCCCTCGACCGTCGCGTAATATTCTTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 GACTIGGTAAGCGCGCAGCACCACGTCGTCGTCGTCATCGCCAACGGGAGTCGTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 15071; 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.2%; Score 26.8; DB 4; Length 505; 14.6%; Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Dumas Mine Edwards, J.B.
APPLICANT: Johnert, S.
APPLICANT: Giordano, J.Y.
ITILE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT PLING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Parent.pm
SEQ ID NO 15539
LENGTH: 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 AAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 27; DB 4
Pred. No. 32;
0; Mismatches
                      CURRENT APPLICATION NUMBER: US/09/358,082A
CURRENT FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: GB 9815879.3
PRIOR PILING DATE: 1998-07-21
PRIOR FILING DATE: 1998-07-21
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: GB 9906712.6
PRIOR PILING DATE: 1999-03-23
PRIOR PRILING DATE: 1999-04-01
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 1999-04-03
PRIOR PILING DATE: 1999-04-03
PRIOR FILING DATE: 1999-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62; Mismatches
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Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.3%;
54.5%;
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 54.5'
Matches 54; Conservative
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Best Local Similarity 14.64
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CRGANISM: Homo sapiens US-09-358-082A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-621-976-15639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-621-976-15639
                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 15071
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 GTGTTTTTTCGGTTCGATACAGATAAAACCCACGTCGATAGCCCTCGACCGTCGCGTAATA 122
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                                                                                                                                                                                                          APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Radie, Lisa
APPLICANT: Radie, Lisa
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikha
APPLICANT: Agostino, Michael J.
IIILE OF INVENTION: SECRETED PROTEINS AND POLYNUCLECTIDES
IIILE OF INVENTION: ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 27; DB 2; Length 2026; Pred. No. 12; 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATER: PATEM: PC-DOS/NS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,228
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29, Application US/09358082A
Patent No. 6589784
GENERAL INFORMATION:
APPLICANT: Antoniou, Michael
APPLICANT: Crombie, Robert
TITLE OF INVENTION: A Polynucleotide
                                                                                                                                             Sequence 3, Application US/08993228
Patent No. 5976838
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELEPHONE: (617) 499-8284
TELEPHONE: (617) 876-8851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                        1356 TTTGTTTGAGTGTGA 1370
175 AAGGGTAGTTAGTGA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.3%;
53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2026 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.3
Matches 57, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-358-082A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Cam
STATE: MA
COUNTRY:
                                                                                                     RESULT 11
US-08-993-228-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-993-228-3
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Gaps

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Sequence 7, Application US/09716865

Sequence 7, Application US/09716865

Sequence 7, Application US/09716865

Sequence 7, Application US/09716865

Sequence 7, Application G548292

SEGUENCE INFORMATION:

APPLICANT: Bramucci, Micheal G

APPLICANT: Nagarajan, Vasantha

APPLICANT: Chen, Mario W

TITLE OF INVENTION: Begradation of Aromatic Compounds

TITLE OF INVENTION: Degradation of Aromatic Compounds

TITLE OF INVENTION: Degradation of Aromatic Compounds

CURRENT FILING DATE: 2000-11-26

PRIOR APPLICATION NUMBER: 60/167,062

PRIOR PELICATION NUMBER: 60/167,062

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Microsoft Office 97

TENGRH: 61/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 GTCGTCGTCATCGCCAACGGGAGTCGTGTTTTCGGTTCGATACAGATAAAACCCACGTC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Covie, Anthony J.
APPLICANT: Fraser, Christopher C.
APPLICANT: Fraser, Christopher C.
APPLICANT: Manning, Stephen
TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
TITLE OF INVENTION: Family and Uses Thereof
FILE REFERENCE: 35800/236924
CURRENT APPLICATION NUMBER: US/09/910,174B
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 09/620,461
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 11.2%; Score 26.8; DB 4; Length 612; 1 Similarity 53.9%; Pred. No. 7.7; 55; Conservative 0; Mismatches 47; Indels
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ilarity 59.0%; Pred. No. 14;
Conservative 0; Mismatches
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LOCATION: (1)...(1975)
CTHER INFORMATION: B7-H2 Short
US-09-910-174B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Pseudomonas CT14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: (70)...(618)
FEATURE:
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Best Local Similarity
Matches 46; Conserva
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Best Local Similarity
Matches 55; Conserv
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US-09-910-174B-3
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553 TATTCTTCAAAAGACACAACAAAAAGACCTGTCACCACAACAAAGGAGGAAGTGAACAGT 612

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Qy 181 AGTIAGTGATACACCGGT 198

Db 613 GCTATCTGAACCTGTGGT 630
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Search completed: September 18, 2004, 13:18:58 Job time : 61.8737 secs

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September 18, 2004, 12:08:47; Search time 263.741 Seconds (without alignments) 4573.952 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/USOT_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 1, Appli	Sequence 14250, A	Sequence 1, Appli Sequence 64, Appl	Sequence 24307, A	Sequence 1632, Ap	Sequence 2, Appli	Sequence 35457, A	Sequence 3. Appli	Seguence 86. Appl	Segmence 40, Appl	Segmence 92822. A	Sequence 203363,
SUMMARIES	US-10-614-282-1 US-10-398-221-3015	US-10-424-599-14250	US-10-320-797-64	US-10-282-122A-24307	US-10-767-701-1632	US-10-390-184-2	US-10-437-963-35457	US-10-390-184-3	US-10-175-523-86	US-10-239-676-40	US-10-437-963-92822	US-10-027-632-203363
	17	13	16	13	17	13	17	13	15	15	17	13
% Query Match Length DB	239	917 273748	3250	696	661	1205	1207	1238	158405	6061	498	616
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ALIGNMENTS

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Sequence 1, Application US/10614282 Sequence 1, Application US/10614282 Publication No. US20040082034A1 GENERAL INFORMATION: APPLICANT: LEE, DUNG-FANG APPLICANT: LEE, DUNG-FANG APPLICANT: JUANG, JYH-LYH TILLE OF INVENTION: INTERNAL RIBOSOME ENTRY SITE OF THE LABIAL GENE FOR TITLE OF INVENTION: PROTEIN EXPRESSION TITLE OF INVENTION: DROTEIN EXPRESSION CURRENT APPLICATION NUMBER: US/10/614,282 CURRENT FILING DATE: 2003-07-08 PRIOR PRILING DATE: 2003-07-08 PRIOR PRILING DATE: 2003-07-08 NUMBER OF SEQ ID NOS: 2 SOFTWARE: PATENTIN VET: 2.1 SEQ ID NO 1 SEG ID NO 1 SEG ID NOS: 2 CURRENT: 239 TYPE: DNA TYPE: DNA ORANISM: Drosophila labial	Query Match Query Match Best Local Similarity 100.0%; Pred. No. 4e-73; Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps	QY 1 ATCAGTCACGACTTGGTAAGCGCGCAGGCAGCACGTCGTCGTCATCGCCAACGGGAG	OY 61 TCGTGTTTTCGGTTCGATACAGATAAAACCCACGTCGATAGCCCTCGACCGTCGCGTAA	OY 121 TATTCTTAGAAAGGAAACGCTAAAGAACTATTTCAAGAACTGTGTGGGAAGTGAAGGGT Db 121 TATTCTTAGAAAGGAAACAGTAAAGAACTATTCAAGAACTGTGTGGCAAGTGAAGGGGT

0;

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APPLICANT: Exemblian, Alexey M.
APPLICANT: Exemblian, Alexey M.
APPLICANT: Exemblian, Carlos
TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 10182-021-999
CURRENT APPLICATION NOMBER: US/10/320,797
CURRENT FILING DATE: 2002-12-16
PRIOR PLILOR DATE: 2001-12-17
RIGHT FILING DATE: 2001-12-17
SUPPRIOR FILING DATE: 2001-12-17
SUPPRIOR FILING DATE: 2001-12-17
SUPPRIOR FILING DATE: 2001-12-17
SUPPRIOR FILING DATE: 2001-13-17
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APPLICANT: Simpson, Andrew
APPLICANT: Reinach, Fernando
APPLICANT: Reinach, Fernando
APPLICANT: Medianis, Joao
APPLICANT: Medianis, Joao
APPLICANT: Arruda, Paulo
TITLE OF INVENTION: Isolated Genome of Xylella Fastidiosa and Uses Thereof
FILE REFERENCE: FABER 20 20 (10213376)
CURRENT APPLICATION NUMBER: US/10/297,465A
CURRENT FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
124 TCTTAGAAAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGGGCAAGTGAAGGGTAGT 183
                                         246 iciliagcalacelactactacadalaggcircalagagatrigcalagiriagalagar 305
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Pred. No. 61;
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                                                                                                  184 TAGTGATACACCGGTTATATCGGA
                                                                                                                                                                                                                                                                       Sequence 1, Application US/10297465A Publication No. US20040142413A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
LENGTH: 2731748
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53.0%;
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ORGANISM: Xylella fastidiosa
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Tocal 70; Conservative
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US-10-320-797-64/c
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Sequence 14250, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFRENCE: 38-21(53223)
CURRENT APLICATION NUMBER: US/10/424;599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 14250
LENGTH: 917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 AACCAAAATTGATAGGCCTCGTCCGTATCGTATAATTCCTTCACACAAAAAGTAAACTA 155
                              181 AGTTAGTGATACACCGGTTATATCGGAGTGGCGAGAAAGTGTGGTTCCGGCTGGACAAT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                         APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
FRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: Patentin Version 3.0
SEQ ID NO 3015
LENGTH: 727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              i LOCATION: (1). (end)
i OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u
US-10-398-221-3015
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Best Local Similarity 61.9%; Pred. No. 1.2;
Matches 52; Conservative 0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; CTHER INFORMATION: Clone ID: FAT_MRT3847_112876C.1
US-10-424-599-14250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32.8;
Pred. No. 1;
                                                                                                                                                                                                      Sequence 3015, Application US/10398221 Publication No. US20040018514A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Listeria monocytogenes 4b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 ACTATTTCAAGAACTG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 GACAAAACAAGATCTG 139
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64.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Glycine max
                                                                                                                                                                                  US-10-398-221-3015/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-10-424-599-14250
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Sequence 1632, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION
APPLICANT: Cao. Vidua
APPLICANT: Cao. Yongwal
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REPERENCE: 38-21(5335)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 1632
LENGTH: 661
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7 GAACAAAGAGAAAATTATTAGAAATTCATAATCTAAAGCAATACTTTAACAAAGGTACT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 CGTCGTCGTCGTCATCGCCAACGGGAGTCGTTTTTTCGGTTCGATACAGATAAAACCCA 93
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US-10-390-184-2

i Sequence 2. Application US/10390184

publication No. US20040053387A1

GENERAL INFORMATION:
APPLICANT: Kumiah Chemical Industry Co., Ltd.
APPLICANT: Hayashi, Hiroaki
ITLE OF INVENTION: A Sieve Tube-Localized Glutathione S-Transferase
FILE REFERENCE: PH-1764 US
CURRENT APPLICATION NUMBER: US/10/390,184

CURRENT FILING DATE: 2003-031-8

PRIOR PLILING DATE: 2003-09-13

PRIOR PLILING DATE: 2002-09-13

NUMBER OF SEQ ID NOS: 11
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Best Local Similarity 57.7%; Pred. No. 4.1;
Matches 56; Conservative 0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 661;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 GTCGCGTAATATTCTTAGAAAGCAAACAGCTAAAGAACTATTTCA 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS27424_1
US-10-767-701-1632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31.4; DB 17;
Pred. No. 3.1;
0; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.1%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 13.1
Best Local Similarity 56.2
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Sorghum bicolor
                                                                         168 GCAAGTGAAG 177
                                                                                                                 67 GCAAGTGAAG 76
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US-10-390-184-2
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SEQ ID NO 2
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: G0/201,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-26
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
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                                                                                                                                                                                                                    67 ITITCGGTTCGATACAGATAAAACCCACGTCGATAGCCCTCGACCGTCGCGTAATATTCT 126
                                                                                                                                                                                                                                                              335 CITCCTCCTCGATCCTACAAGAACGAAGAAGAACTCCACCATACGCATCTTTCCC 276
                                                                                                                   7 CACGACTIGGTAAGCGCGCAGCAGCACGTCGTCGTCGTCATCGCCAACGGGAGTCGTGT
                                                                            Gaps
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                                                                         0;
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                     Length 3250;
                                                                      65; Indels
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13.2%; Score 31.6; DB 13; Length
Best Local Similarity 65.7%; Pred. No. 3.2;
Matches 46; Conservative 0; Mismatches 24; Indels
                     DB 16;
                                                                    0; Mismatches
                  Score 32;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24307, Application US/10282122A Publication No. US20040029129A1
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ORGANISM: Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                           127 TAGAAAGCAAACAGCT 142
                                                                                                                                                                                                                                                                                                                                                                          275 TATACAACATATCCCT 260
                     13.4%;
52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                    71; Conservative
                                            Best Local Similarity
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                     Query Match
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                                                                    Matches
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CGTCGATAGCCCTCGACCGTCGCGTAATATTCTTAGA 130

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108 GACCGTCGCGTAATATTCTTAGAAAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGTG 167

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Gaps

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APPLICANY: Laeng, Pascal
APPLICANY: Laeng, Pascal
APPLICANY: Laeng, Pascal
APPLICANY: Bajan, Prithi
APPLICANY: Rajan, Prithi
APPLICANY: Rajan, Prithi
APPLICANY: Rajan, Prithi
APPLICANY: Rajan, Prithi
APPLICANY: Rajan, Prithi
APPLICANY: Rajan, Prithi
APPLICANY: Rajan, Prithi
APPLICANY: Rajan, Prithi
APPLICANY: NUMBER: US 60/299,151
PRICR APPLICANION NUMBER: US 60/299,151
PRICR APPLICANION NUMBER: US 60/317,828
PRICR APPLICANION NUMBER: US 60/317,828
PRICR FILING DATE: 2001-09-07
PRICR PILING DATE: 2001-09-07
PRICR APPLICANION NUMBER: US 60/333,047
PRICR APPLICATION NUMBER: US 60/349,936
PRICR FILING DATE: 2002-01-18
PRICR FILING DATE: 2002-01-18
PRICR FILING DATE: 2002-01-18
PRICR FILING DATE: 2002-01-18
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PRICR FILING DATE: 2002-01-18
PRICR FILING DATE: 2002-01-18
PRICR FILING DATE: 2002-01-18
PRICR FILING DATE: 2002-01-18
PRICR FILING DATE: 2002-01-18
PRICR FILING DATE: 2002-01-18
PRICR FILING DATE: 2002-01-04
NUMBER OF SEQ ID NOS: 197
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APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
APPLICANT: BERLIN, Kurt
APPLICANTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019058.8
DE 10019058.8
DE 1003529.7
DE 1003529.7
DE 10043826.1
PRIOR FILING DATE: 2001-04-06
2000-04-06
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  94 CGICCATAGCCCICGACCGICGCGIAAIAITCITAGA 130
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                                                                                                                                                                                        ; Sequence 86, Application US/10175523; Publication No. US20030096264A1
GENERAL INFORMATION: APPLICANT: BROCKMAN, Jeffrey
                                                                                                                                                                                                                                                                                                       Evans, David
Hook, Derek
Klimczak, Leszek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Mus musculus
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SEQ ID NO 86
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US-10-239-676-40/c
                                                                                                                                     RESULT 11
US-10-175-523-86
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                                                                                                                                        Sequence 35457, Application US/10437963
; Sequence 35457, Application US/10437963
; Sequence 35457, Application US/20040123343A1
; Sequence 35457, Application No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Ross, Thomas J.
; APPLICANT: Cao, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Brabauk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION (Plants)
; TITLE OF INVENTION (Plants)
; TITLE OF SERRICE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 35457
; LENGTH: 1207
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APPLICANT: Hayashi, Hiroaki
TITLE OF INVENTION: A Sieve Tube-Localized Glutathione S-Transferase
FILE REFERENCE: PH-1764 US
CURRENT APPLICATION NUMBER: US/10/390,184
CURRENT FILING DATE: 2003-03-18
PRIOR FILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.1%; Score 31.4; DB 17; Length 1207; 57.7%; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Indels
1095 CTGCTGTTGGTGAATTCCGAGTGGTCACATTATTATA 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 CGTCGATAGCCCTCGACCGTCGCGTAATATTCTTAGA 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: PAT_MRT4530_39375C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/10390184 Publication No. US20040053387A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-390-184-3
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111 CGTCGCGTAATATTCTTAGAAAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGGGCA 170
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ITTLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITTLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/027,632
FRIOR APPLICATION NUMBER: US/0218,006
FRIOR FILING DATE: 2000-07-12
FRIOR FILING DATE: 2000-07-12
FRIOR FILING DATE: 2000-03-29
FRIOR APPLICATION NUMBER: US/01/193,483
FRIOR APPLICATION NUMBER: US/01/193,483
FRIOR APPLICATION NUMBER: US/01/167,363
FRIOR APPLICATION NUMBER: US/01/167,363
FRIOR FILING DATE: 1999-11-23
FRIOR APPLICATION NUMBER: US/01/167,363
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-08-08
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Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 AGTGAAGGGTAGTTAGTGATACACCGGTTATATCGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.6%; Score 30.2; DE ilarity 56.6%; Pred. No. 7.8; Conservative 0; Mismatches
                                                   CURRENT FILING DATE: 2002-04-30
PRIOR FILING DATE: 2000-04-30
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
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56.6%;
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US-10-027-632-203363
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SEQ ID NO 203363
LENGTH: 616
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SEQ ID NO 203363
LENGTH: 616
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Best Local 6
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 CGCGCAGGCACGTCGTCGTCGTCATCGCCAACGGGAGTCGTGTTTTTCGGTTCGATA 80
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICATI Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                            OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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                                                                                                                                                                                                                                                                                                                               Length 6061;
                                                                                                                                                                                                                                                                                                                            Score 31; DB 15; Length 60 Pred. No. 13; 0; Mismatches 25; Indels
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Pred. No. 7;
0; Mismatches 33;
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US-10-437-963-92822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 92822, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbaruk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.6%;
60.2%;
                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 64.8%;
Matches 46; Conservative
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Best Local Similarity 60.2°
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2000-04-07
2000-06-30
2000-09-01
NUMBER OF SEQ ID NOS: 228
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ORGANISM: Oryza sativa
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US-10-027-632-203363
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LENGTH: 498
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LENGTH: 6061
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BX420094 BX420094
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BX542182 Leishmani
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BX5983355 ZM0264C01
AF227817 ICtalurus
BU794358 WHE4103 A
BU57817 Ser18e10.7
BH465834 BOHJI55TR
BU901940 AGENCOURT
BX13003 Danio rer
CD649081 AUF 104 I
CD048532 AGENCOURT
BX13107 AL573127
AUG77131 AUG77131
BI561029 603254230
BG616128 602642702
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Total number Minimum DB Maximum DB

Database

Result No.

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Searched:

Sequence:

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BI375946 STO DOSOPHIA MENA linear EST 01-AUG-2001 REG3854.5prime RE Drosophila melanogaster normalized Embryo pFlc-1 Drosophila melanogaster cDNA clone REG3854 5, mRNA sequence.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Behydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 510)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B.,
Carlson, J., Champe, M., Chaver, C., Dorsett, V., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G.,
Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Phouannavong, S., Man, K., Yu, C., Lewis, S.E., Celniker, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (fruit fly)
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                                                           AZ581975
LBAF025H06
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AF227817
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BU578178
AM133037
BE803253
BQ725287
BH465834
BU301940
BX139003
CD649081
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CD64913
BX492451
CE691717
BB941338
AL573127
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BDGP/HHMI RE Drosophila EST
"memblished (2001)
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                                                                                                                                                                               September 18, 2004, 10:33:16; Search time 2018.88 Seconds (without alignments) 3535.155 Million cell updates/sec
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AU273213 AU273213 AZ760934 1M0555E02 CA413042 ULH-EZD-BQ952602 AGENCOURT AU082434 AU082434 AZ404419 1M0172023 AW448889 BRY 1810 BP657587 OVZ 17 AO AU082410 AU082410 CD233195 SSL_12_E0

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BW068571 Nori Satch unpublished cDNA library, cleaving embryo Ciona intestinalis cDNA clone rcicl075j03 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="rcicl075j03"
/tissue type="whole body"
/dev_stage="cleaving embryo"
/clone lib="Nori Satch unpublished cDNA library, cleaving embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 AACGGGAGTCGTGTTTTCGGTTCGATACAGATAAAACCCACGTCGATAGCCCTCGACCG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Entebobranchia; Cionidae; Ciona.
1 (bases 1 to 162)
Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona intestinalis (2002c)
                                                                                                                                                                                                                                                                                                                                                                                                                                         924 geracecegecadeceraarercegecercegecececacecaceacacarareaecer 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 TCGATACAGATAAAACCCACGTCGATAGCCCTCGACCGTCGCGTAATATTCTTAGAAAGC 134
                                                                                                                               /tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/clone_lib="Drought"
/note="Vector: Lambda Zap; Contains a mixture of entire plantlets harvested in a series of days-post-watering timepoints."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             804 GAGTTATGACAGGATAGATAGAGAAGTATATACAAAATGAAACGATAGGGGGAATAC 747
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Pred. No. 3;
0; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: satch@ascidian.zcol.kyoto-u.ac.jp.
Location/Qualifiers
                         l. .1138
/organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2002)
Contact: Nor! Satch
Copartment of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Fax: 81-75-753-4081
                                                              /mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF087E01DT"
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BW068571
BW068571.1 GI:24169983
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Best Local Similarity 50.6%;
Matches 90; Conservative
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                              source
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VERSION
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AUTHORS
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BW068571
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                                                                                                                                                                                                                                                                                                                                                        Anote="Organ: embryo; Vector: pFlc1; Site_1: XhoI; Site_2: BamHI; Library was Kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BQ144508 1138 bp mRNA linear EST 24-APR-2002
NF087E01DT1F1005 Drought Medicago truncatula cDNA clone NF087E01DT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 1138)

Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library
Unpublished (2000)
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                                                                                                                                                                                                                       /sex="male and female"
/dev stage="0-24 hours mixed stage embryonic"
/lab_host="DH5-alpha TonA"
/clone lib="RE Drosophila melanogaster normalized Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTIAGIGAIACACCGGTIAIAICGGAGIGGCGAGAAAGIGIGGIICCGGCIGGACAAI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATTCTTAGAAAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGTGGCAAGTGAAGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003674: arm:3R [2306679,2604706]
estimated-cyto:83F1-84A5: 05/16/2001
Plate: RE 638 row: E column: 6
High quality sequence stop: 453.
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0
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Plant Balology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
                                                                                                                                                             organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 239; DB 12; 100.0%; Pred. No. 8.2e-64;
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Fax: 580 221 7390
Email: gdmay@noble.org
Insert Length: 1138 Std Brror: 0.00
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Seq primer: TCACACAGGAAACAGCTATGAC.
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Medicago truncatula
                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:7227"
/clone="RE63854"
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BQ144508
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                                                                                                                                        1. .510
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Best Local Similarity
Matches 239; Conserv
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                                                                                                                                          source
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BQ144508/c
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BX420094.1 GI:30638109
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57.3%;
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(bases 1 to 625)
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BX420094/c
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16S rRNA, mRNA
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         TTCCAAAAATGNAAAAAGCAAAATNCCCAACCCCCTTGTNACGAGGTGGTTTACAAG 121
                                                                                                                                                                                                                                                                                                                                                                                                                      Gross, P.S., Bartlett, T.C., Browdy, C.L., Chapman, R.W. and Warr, G.W. manue gene discovery by expressed sequence tag analysis of hemocytes and hepatopancreas in the Pacific White Shrimp, Litopenaeus vannamei, and the Atlantic White Shrimp, L. setiferus Dev. Comp. Immunol. 25 (7), 565-577 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 GCGTAATATTCTTAGAAAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGTGGCAAGTG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 GCGTAATCTTCTTTGAGAGTCCACATCGNCAGGAAGGGGTTGCGACCNCGATGNTGAATN 307
                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca,
manalacostraca; Eucarida, Decapoda; Dendrobranchiata, Penaeoidea,
Penaeidae, Litopenaeus.
1 (bases 1 to 496)
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Crassostrea virginica
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Ostreoida;
Ostreoidea; Ostreidae; Crassostrea.
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AUF_102_H24_T7 Crassostrea virginica Gill Crassostrea virginica CDNA 5' similar to Unknown, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="Vector: pTriplEx2; Site_1: Sfi I; Site_2: Sfi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Gross PS, Bartlett TC
Department of Biochemistry and Molecular Biology
Medical University of South Carolina
Box 250509, 173 Ashley Avenue, Charleston, SC 29425,
Tel: 846 792 9935
Fax: 843 792 4850
                                                                                                                                                                                                       BF024030 496 bp mRNA linear PvP 300 L99-29 Litopenaeus vannamei cDNA similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 496;
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                                                                                                                                                                                                                                                                                                                 Litopenaeus vannamei (Pacific white shrimp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Litopenaeus vannamei"
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ilarity 57.1%; Pred. No. 6.4;
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:6689"
/tissue_type="Hepatopancreas"
/clone_lib="159-29"
                                                                                                                   AGAGCAACTGTGGGTTAAACACCGGTTA 149
                                                                                173 TGAAGGGTAGTTAGTGATACACCGGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                  Litopenaeus vannamei
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Best Local Simi
Matches 56;
                                            62
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KEYWORDS
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CD648340/c
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TITLE
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PUBMED
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BF024030
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Peatman, E., Kucuktas, H., Li, P., He, C., Feng, J., Wei, X. and Liu, Z. Differentially expressed oyster (Crassostrea virginica) genes after exposure to mercury Unpublished (2003)
                                                                                                                             Contact: Liu ZJ
The Fish Molecular Genetics and Biotechnology Laboratory,
Department of Fisheries and Allied Aquacultures and Program of Cell
and Molecular Biosciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:6565"
/clone_lib="Crassostrea virginica Gill"
/note="Organ: Gill; Vector: pSport1; Site_1: Not1; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ÷
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)
1 (bases 1 to 201)
1 (bases 1 to 1201)
Full-length cDNA libraries and normalization
Unpublished (2001)
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cgi-bin/cluster.cgi?seq=CSODF023DC0SQP1&cluster=2290.f. Contac
Feng Liang Email: fliang@lifetech.com URL http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF023DC0SQP1.
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2290.f.
more information about this cluster, see
                                                                                                                                                                                                                                           Auburn University
203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
213 Swingle Hall, Auburn University, Auburn, AL 36849, USA
FAX: 334 844 9208
Email: zliu@acesag.auburn.edu
Seq primer: M13 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 GATACACCGGTTATATCGGAGTGGCGAGAAAGTGTGGTTCCGGCTGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              285 AAGAAACTACATTICITTIGAAGTTCGATATACTGATGTTCCTGCGTGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Crassostrea virginica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34.8; DI
Pred. No. 7.9;
0; Mismatches
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/tissue type="FETAL BRAIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
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/db_xref="taxon:9606"
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymurcleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWMD42 (gil4732114 |gb|AF129702.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
2 (bases 1 to 670)
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Best Local Similarity
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ORGANISM
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AUTHORS
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KEYWORDS
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/lab_host="E. Coli strain XLI0-Gold, T1-resistant, F-"
/lab_host="E. Coli strain XLI0-Gold, T1-resistant, F-"
/clone_lib="Mouse lobb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
                            /clone_lib="Mono sapiens FETAL BRAIN"
//oloe="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
ass primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                  85 TAAAACCCACGTCGATAGCCCTCGACCGTCGCGTAATATTCTTAGAAAGCAAACAGCTAA 144
                                                                                                                                                                                                                                                                                                                                                            SS8. KAAAACCBAMKWAAAKACBAAKKKRAABCBCBAKKKKKAABBBKCKDAAAKKKCBAKKCA 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 563)
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1M0370K21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0370K21 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacres, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                              14.6%; Score 34.8; DB 13; Length 1201; 24.5%; Pred. No. 9.6;
                                                                                                                                                                                                                                                                                  54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 GGAGTGGCGAGAAGTGTGGTTCCGGCTGGACAAT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : |:::|:|:| : : :|:| :::| 838 KAAKKAAKCAAAAAK 804
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                                                                                                                                                                                                                                                                                  63; Mismatches
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Class: plasmid ends
High quality sequence stop: 563.
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0370K21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            row: K column: 21
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Insert Length: 10000 Std Erro
            'dev_stage="fetal"
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Unpublished (2000)
                                                                                                                                                                                                                                                                                    38; Conservative
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .563
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84112, USA
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                                                                                                              83 GATAAAACCCACGTCGATAGCCCTCGACCGTCGCGTAATATTCTTAGAAAGCAAACAGCT
                                                                                                                                                                      286 GCTTAACCACAGAGCCATCTCCCCAGGCCTCCTGGAAGTAAACTTTTAAACCACACACTTTT
                                                                                                                                                                                                                                25 CAGGCAGCACGTCGTCGTCGTCATCGCCAACGGGAGTCGTGTTTTCGGTTCGATACAGA
                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LBAF025H06 670 bp DNA linear GSS 20-JUM
Leishmania braziliensis GSS, clone LBAF025H06, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (17-UUN-2003) Cruz A.K., University of Sao Paulo,
Department of Molecular and Cell Biology, FMRP, Avenida
Bandeirantes 3900, Ribeirao Preto, SP, 14049-900, BRAZIL
                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae,
Leishmania, Leishmania braziliensis species complex.
     Length 563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 670;
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                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Leishmania braziliensis"
Query Match 14.5%; Score 34.6; DB 28; Best Local Similarity 51.3%; Pred. No. 8.9; Matches 79; Conservative 0; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29;
                                                                                                                                                                                                                                                                                                                                         203 TCGGAGTGGCGAGAAGTGTGGTTCCGGCTGGAC 236
                                                                                                                                                                                                                                                                                                                                                                                                406 NAAGCTAGAAGAAGATGTGACCCCGGGGCTGGTC 439
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/strain="MHOM/BR/75/M2904"
/db_xref="taxon:5660"
/clone="LBAF025H06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone requests: akcruz@fmrp.usp.br
Location/Qualifiers
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Leishmania braziliensis
Leishmania braziliensis
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Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 86F3. 86F3 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene, Further details:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ983355 638 bp DNA linear GSS 27-APR-2001
2M0264C01R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0264C01 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 TCGCGTAATATTCTTAGAAAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGTGGCAAG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396 IGTITITATTATTATTAAAAAAAAAAAAGATGTTAGAATAAAATTATACAAATATTTGGGAAA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I toi A3.)

Ilan, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhaussern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 AATGCGTGCAGTCATTTTGACCGTTGGTCATTTAAGGGACAGATACATAGAACTCTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 AACGGGAGTCGTGTTTTCGGTTCGATACAGATAAAACCCACGTCGATAGCCCTCGACCG
                                                                                                                                                                                                                                                                                                                                                                                                          Length 507;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    456 AGTCAGTGAATTATAGCTATATGGGTTTTATTTGAAT 492
                                                                                                                                                                                                                                                                                                                                                                                                          DB 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 77;
                                                                                                                                                         http://www.sanger.ac.uk/Projects/D rerio/
                                                                                                                                                                                                                    /organism="Danio rerio"
/mol_type="genomic DNA"
db_xref="taxon:7955"
/clone="DKBY 86F3"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                     Score 33.8; DB Pred. No. 15; 0; Mismatches
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
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/strain="C57BL/6J"
                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
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ilarity 51.0%;
Conservative 0
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Best Local Simi
Matches 80;
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AZ983355
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BX137891
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                    144
                                                          210 CCCAGCTCAGATCGAGTACGCTTCCCAGGCCCACCAGGGTCTTCGGTACCTGCGAGGTCA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 CATACACCGCGACGTCGTCCCCTCGGCCACAACATACGTGGTGGCGTGGCTTGCCGCGTA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 TAAAACCCACGTCGATAGCCCTCGACCGTCGCGTAATATTCTTAGAAAGCAAACAGCTAA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 CCCAGCTCAGATCGAGTACGCTTCCCAGGCCCACGGGTCTTCGGTACCTGCGAGGTCA 151
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1 (bases 1 to 507)
Humphray, S.J., Huckle, E. and Durham, J.L.
                85 TAAAACCCACGTCGATAGCCCTCGACCGTCGCGTAATATTCTTAGAAAGCAAACAGCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 CAGGCAGCACGTCGTCGTCGTCATCGCCAACGGGAGTCGTGTTTTTCGGTTCGATACAGA
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                                                                                                                                                                                                                                                                DNA linear GSS 20-JU
LBAF025H09, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (17-JUN-2003) Cruz A.K., University of Sao Paulo, Department of Molecular and Cell Biology, FMRP, Avenida Bandeirantes 3900, Ribeirao Preto, SP, 14049-900, BRAZIL Clone requests: akcruz@fmrp.usp.br.
                                                                                                                                                                                                                                                                                                                                                                    GSS; genomic survey sequence.
Leishmania braziliensis
Leishmania braziliensis
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania; Leishmania braziliensis species complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laurentino, E.C., Ruiz, J.C. and Cruz, A.K.
GSS analysis of the Leishmania braziliensis genome
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Leishmania braziliensis"
/mol_type="genomic DNA"
/strain="MHOM/BR/15/M2904"
/db xref="taxon.5660"
/clone="LBAP025HO9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 29;
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Leishmania braziliensis GSS, clone
                                                                                                                                                150 CCCAGTCTTCCATGCACTTTGTAGCA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 AGAACTATTTCAAGAACTGTGGGCA 170
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Danio rerio
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                                                                                                                                                                                                                                                                                                          sequence.
BX542273
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Query Match
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                    ORIGIN
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                                                                                                                                                                                                                                                                                                             dd
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                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                             10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of FWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTC 23-JAN-2003
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1 (bases 1 to 1026)

Kim, S., Li, P., Zheng, X., Dunham, R.A. and Liu, Z.
Gene expression in the muscles of young and mature channel caffish (Ictalurus punctatus) as analyzed by expressed sequence tags and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                               /lab_host="E. coli strain XLI0-Gold, Tl-resistant, F-"
clone lib= Mouse lokb plasmid UUGC2M library"
/note="Wector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310 AAAGCACAGTTCCAAAAATCTATTAAAACTACTGTGGTGCTAATAAAGAATTGTTAGATA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="muscle"
<11...1026
/note="similar to mitochondrial long-chain enoyl-CoA
hydratase/3-hydroxyacyl-CoA dehydrogenase; coding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (21-JAN-2000) Fisheries and Allied Aquacultures and the Program of Cell and Molecular Biosciences, Auburn University, 203 Swingle Hall, Auburn, Al 36849, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hydratase/3-hydroxyacyl-CoA dehydrogenase mRNA, partial sequence
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Ictalurus punctatus mitochondrial long-chain enoyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adaptored vector DNA, and transformed into
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 28;
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Fish Physiol. Biochem. (2003) In press
                                                                                                                                                                    Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33.6; I
Pred. No. 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 rarrcrererarrregaaaaccraraa 397
db xref="taxon:10090"
                    clone="UUGC2M0264C01"
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/db_xref="taxon:7998"
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1 Similarity 61.4%;
54; Conservative
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Liu, Z. and Kim, S.
Direct Submission
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Best Local Similarity
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AF227817/c
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TITLE
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// (AD LYPRE="MRNA"
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// (AD xref="taxon:4565"
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// (Adev_stage="Full tillering"
// (Adev_stage="Extressed root cDNA library"
// (AD Lib="Wheat salt-stressed root cDNA library"
// (AD Lib="Wheat salt-stressed root conting the plants grown to full tillering stage were treated with 150 mW Nacl for either 12 hours or 7 days. Root tissues of the plants subjected to both types of treatment were collected separately at University of California, Davis (B. Akhunov and K. Deal in J. Dvorak's Lab). Total RNA was prepared separately from the two samples (12h and 7day treatments), and equal amount of RNA was then pooled. PolyA RNA was purified from the pooled RNA, a cDNA library was made, and the cDNA clones were in vivo excised to give platuescript SK(-) phagemids in J. Dvorak's lab (B. Akhunov, J. Dvorak) at the University of California, Davis. Colony plating, plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2002)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA
Par: 510559573
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                                                                                                                                     852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.

( bases 1 to 537)
Anderson, O.D., Akhunov, E., Chao, S., Crossman, C., Deal, K.,
Dvorak, J., Lazo, G.R., Pham, J., Rausch, C.J., Wilson, C. and Woo, J.
The structure and function of the expressed portion of the wheat
genomes - Salt-stressed root cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BQ743358
WHE4103 AlO B19ZS Wheat salt-stressed root cDNA library Triticum aestivum cDNA clone WHE4103_AlO_B19, mRNA sequence.
                                                                                                                                                                                                  911 CCCTTCTGTAGAACTCTTAGATCACACACCACCCTTCGGAACGATTTTAGGAACTGTGTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: oandersn@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer.
                                                                    .
0
Length 1026;
                                                                    Indels
   DB 11;
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/organism="Triticum aestivum"
14.0%; Score 33.4; I
65.3%; Pred. No. 25;
                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                              170 AAGTGAAGGGTAGTT 184
                                                                                                                                                                                                                                                                                                                                                   837
                                                                        49; Conservative
                                                                                                                                                                                                                                                                                                                                                   851 AAGAGAAATGTCGGT
                                    Best Local Similarity
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/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
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61.9%;
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Local Sa.
52;
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AW133037
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Xho1; The CDNA library was constructed from mRNA isolated
from 9-11 day old seedlings that were induced for HR
(hypersensitive response) by vacuum infiltrating plant
tissue with Pseudomonas syringae pv. glycinea carrying the
avrB gene (Genetics 141:1597-1664). Plant tissue (expanded
unifoliate leaves) was collected at 2, 4, 8, 12, 24, 35,
and 53 hrs after inoculation and their mRNA pooled equally
for CDNA construction. The library was prepared using the
Stratagene pBluescript II SK(+) library construction kit.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with an Xhol restriction
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Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hiller,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allon,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BU578178 349 bp mRNA linear BST 17-SEP-2002 sar48g12.yl Gm-c1074 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1074-5711 5' similar to TR:080921 080921 PUTATIVE RNA-BINDING
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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/tissue type="seedlings induced for HR (hypersensitive
response)"
                                                                                                                                                      23 CGCAGGCAGCACGICGICGICGICAICGCCAACGGGAGICGIGITITICGGITCGAIACA
                                                                               Gaps
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
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           Length 537;
                                                                                   Indels
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       DB 13;
                                                                                   38;
                                                                                                                                                                                                                                                                                                         83 GATAAAACCCACGTCGATAGCCCTCGACCGTCGC 116
                                                                                                                                                                                                                                                                                                                                                                                     134 ACGGTACAGCAGGAGGAGGACCCCGGTCGTTGC 167
   Score 33.2; DB
Pred. No. 24;
0; Mismatches
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/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID:
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/lab_host="DH10B"
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High quality sequence stop: 295.
Location/Qualifiers
1...349
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BU578178
BU578178.1 GI:23057504
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   13.9%;
59.6%;
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Query Match
Best Local Similarity
Matches 56; Conserv
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COMMENT

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"I (Dameser I to 418)
"S Shoemaker, R. , Keim, P. , Vodkin, L. , Erpelding, J. , Coryell, V. ,
Khanna, A., Bolla, B., Marra, M., Hillier, L. , Kacaba, T. , Martin, J. ,
Edeck, C., Wylle, T. , Underwood, K. , Steptoe, M. , Theising, B., Allen, M.,
Bowers, Y. , Person, B. , Swaller, T. , Gibbons, M. , Pape, D. , Harvey, N. ,
Schurk, R., Watter, E., Kohn, S., Shin, T. , Jackson, Y., Cardenas, M.,
McCann, K., Watterston, R. and Wilson, R. ,
Unpublished (1999)
Contact: Shoemarker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forset Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA insert is protected from XhoI digestion on a methylation during first strand synthesis. The cDNA fragments were directionally cloned into the EcoRI. XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into B.coli ElectroMax DHIOB host cells. Plant care, incoulations, and library construction were performed by Steve Clough (Lila Vodkin lab, University of Illinois)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sel3e10.yl Gm-c1013 Glycine max cDNA clone GENOWE SYSTEMS CLONE ID: Gm-c1013-3427 5' similar to TR:Q9ZUR6 Q9ZUR6 PUTATIVE RNA BINDING AW133037
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids; eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 TCTTAGAAAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGTGGCAAGTGAAGGGTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 rcttagcaaacgtactactacagaaaggcttcgagagggggttgcaaagtttggtgaagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="GENOME SYSTEMS CLONE ID: Gm-c1013-3427"
/tissue_type="Whole seedlings, 2-3 week old seedlings,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32.8; I
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Glycine max"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTCATGCAAGGGTTGTAACTGA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             greenhouse grown"
/lab_host="XL10-Gold"
/clone_lib="Gm-c1013"
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Seg primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 TAGTGATACACCGGTTATATCGGA
```

XhoI, This cDNA library was constructed from mRNA isolated from whole seedlings of 2-3 week old greenhouse grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR cDNA library construction kit.
Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XIIO-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding."

ORIGIN

124 TCTTAGAAAGCAAACAGCTAAAGAACTATTTCAAGAACTGTGTGGCAAGTGAAGGGTAGT 183 Gaps 0; Query Match
Best Local Similarity 61.9%; Pred. No. 30;
Matches 52; Conservative 0; Mismatches 32; Indels 0 δ

184 TAGTGATACACCGGTTATATCGGA 207

273 TGTTCATGCAAGGGTTGTAACTGA 296

Search completed: September 18, 2004, 13:16:48 Job time : 2023.88 secs

213 TCTTAGCAAACGTACTACAGAAAGGCTTCGAGAGGAGTTTGCAAAGTTTGGTGAAGT 272

qq δ

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM MUCIEIC - III	om muciero - muciero searon, using sw model	
Run on:	September 18, 2004, 09:46:06; Search time 1166.45 Seconds (without alignments) 9066.559 Million cell updates/sec	
Title: Perfect score: Sequence:	US-10-614-282-2 244 1 agcgccggggatttaaatgcaccaggtcactcagtgacag 244	
Scoring table: IDENTITY_NUC	IDENTITY NUC	

6940544 3470272 seqs, 21671516995 residues Total number of hits satisfying chosen parameters: Gapop 10.0 , Gapext 1.0 Minimum DB seq length: 0 Maximum DB seq length: 200000000 Searched:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	ult No.		Ouerv				
1		Score	Match	Length	DB	ID	Description
	1	1 :	1	1	i.		
	٦.	24	100.0	0271		AC004079	04079 Homo
	(1)	42.	99.3	702	σ	AC142285	42285 Pan
	m	40.	98.7	919	0	AC146102	46102 Pan t
	4	04.	83.9	288	N	AC129963	9963 Sus
	Ŋ	199.2	81.6	Ŋ	10	AC116662	116662 Rat
	9	99.	81.6	346	~1	AC097087	7087 Rattus
	7	99.	81.6	988	~	AC122669	569 Rattus
	c o	æ	75.4	900	~1	AC015583	583
	σ	8	75.4	362	~	AC091106	106 Mus
	10	18	75.4	368	N	AC123672	572 Mus
υ	11	72.	70.7	М	9	AX344703	1703 Segu
	12	135.2	55.4	6118	9	AX344702	702 Seque
	13	ω	25.4	S	σ	BC032547	Homo sa
	14	53.8	22.0	N	10	MUSERA1A	M22115 Mouse ERA-1
	15	51	20.9	4	٦	MUSHOX	M20214 Mus musculu
U	16	4	18.0	099	N	on.	Siluran
	17	ä	17.0	605		289	AL928943 Mouse DNA
	18	0	16.7	046		99	AC120995 Rattus no
บ	19	40.8	16.7	0		AC112571	AC112571 Rattus no
	20	ω.	15.9	581		コ	AP003414 Oryza sat
	21	ω,	15.9	159761	œ	2	
	22	38	15.6	41	σ	걾	AL359316 Human DNA
υ	23	38	15.6	8	9	AX335531	AX335531 Sequence
	47.	m,	15.6	324604	σ,	U82671	兒
	52	· .	15.5	77	Н	AF210249	
U	9 17	٠.	15.4	44	7	AC147476	_
	7.7	<u>- 1</u>	15.3	215259	~ ;	AC118349	AC118349 Rattus no
	0 C	~ t	15.2	617	_	PM78128	`
	, נע ע נע	~ t	15.2	3050		AX./46./3./	7
	0.0	37.2	15.2	ا (س		AK091024	S OMC
	77	_	15.2	174367	$\overline{}$	AL512597	97
	2 6	3.7	15.2	91		AE007075	
	£ .	3.7	15.2	· (1	9	525	Sedne
	34	37	15.2	63	6	999	Homo
υ	35	37	15.2	72	Φ	N	Homo
	36	37	15.2	9	Н	33	lycob
	37		15.2	48	15	BX842579	Bx842579 Mycobacte
	38	9	15.1	-	10	П	use
υ	39	9	15.0	72	σ	AC007220	\circ
	0.4	9	15.0	85	σ	9	Homo
	41	9	15.0	0689	10	-	39152 Mus
υ	42	ė,	15.0	5385	7	9682	Rattu
	43	36.6	15.0	257407	N	AC109870	9870 Ra
	44	ġ	15.0	5831	7	2777	7770 Rattus
υ	45	9	15.0	6634	~	9660	AC109963 Rattus no

ALIGNMENTS

RESULT 1	
ACCO40/9/C	AC004079 102717 bp DNA linear PRT 26-APR-2003
DEFINITION	iens PAC clone RP1-167F23 from 7
ACCESSION	AC004079
VERSION	AC004079.1 GI:2822174
KEYWORDS	HTG.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 102717)
AUTHORS	Sulston, J.E. and Waterston, R.
TITLE	Toward a complete human genome sequence
JOURNAL	Genome Res. 8 (11), 1097-1108 (1998)

Waterston, R.

AUTHORS TITLE JOURNAL

AUTHORS TITLE

REFERENCE

JOURNAL

AUTHORS JOURNAL

REFERENCE

TITLE JOURNAL REFERENCE

MEDLINE PUBMED AUTHORS

REFERENCE

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/allele="A"
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3333. .3696
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3697. .3799
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1926. .5064
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6427. .6546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="MER1_type"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3697. .3799
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i572_ .6868
'rpt_family="Alu"
                                                                                                                                                                                                            rpt_family="L1"
.099. .1412
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                                                                                          chromosome="7"
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source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (26-APR-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                 Department of Genetics, Washington
Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                     Department of Genetics, Washington
Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington
Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTICE: This sequence may not represent the entire insert of this folds. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEIGHBORING SEQUENCE INFORMATION:
The actual start of this clone is at base position 1 of RPI-167F23
the actual and is at base position 102717 of RPI-167F23. The
orientation of this clone is unknown.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone was derived from human PAC library RPCI-1, prepared by Pieter de Jong and coworkers at http://www.chori.org using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Washington University Genome Sequencing Center
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                                                                 Duckels,G., Hawkins,M., Hinds,K. and Jones,K.
The sequence of Homo sapiens PAC clone RP1-167F23
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Genetics,
Park Avenue, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Center
                                                                                                                                                                                        Direct Submission
Submitted (29-JAN-1998)
University, 4444 Forest
4 (bases 1 to 102717)
                                                                                                                                                                                                                                                                                                                                                       University, 4444 Forest 5 (bases 1 to 102717) Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (04-FBB-2000)
University, 4444 Forest
6 (bases 1 to 102717)
                                                                                                                                                                                                                                                                                                                                       Submitted (03-FEB-2000)
                                             (bases 1 to 102717)
                                                                                                                 Unpublished (2001)
3 (bases 1 to 102717)
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                                                                                                                                                                                                                                                                                  Waterston, R.
Direct Submission
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Waterston, R.

TITLE JOURNAL

COMMENT

REFERENCE

FEATURES

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The RPCI-43 BAC Library has been constructed by Chung-Li Shu. DNA was isolated from white blood cells obtained from a male chimpanzee (Pan troglodytes, 'Clint', Yerkes #CQ471; birthdates 6-6-80). The clone and detailed information can be obtained from ResGen (http://www.resgen.com) or Pieter de Jong and co-workers at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTICE: This sequence may not represent the entire insert of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                           Wilson,R.K.
Direct Submission
Submitted (27-MAR-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 170237)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson,R.
Direct Submission
Submitted (26-SEP-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------ Genome Center
Center: Washington University Genome Sequencing Center
                                                            Mammalia; Butheria; Chordata; Craniata; Vertebrata; Bute: 1 (bases 1 to 170237)
Belter; E. and Maupin, R.
The semiacro.
                                                                                                                                                                   The sequence of Pan troglodytes BAC clone RP43-169B4 Unpublished (2001)
2 (bases 1 to 170237)
Sulston, J.E. and Wilson, R. Sequencing of Pan troglodytes
Unpublished (2001)
3 (bases 1 to 170237)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Data from RP43-21L13 was used to finish this clone.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is the entire insert of the clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
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/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: C_PT169B04
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                                                       Pan troglodytes
Eukaryota; Metazoa; Chordata;
                                    Pan troglodytes (chimpanzee)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.bacpac.chori.org.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: WUGSC
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            KEYWORDS
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AC142285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 GGAGGAAGTGAGAAAGTTGGCACAGTCACGCCGGGCTTCGCAGGACCAGGTCACTCAGTG
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                                                                                                                                                                                                                                                       /allele="C"
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/db_xref="dbSNP:2522829"
/10400.10406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /allele="C"
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10666
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85447.8579
/rpt_family="AT_rich"
                                                                                                                                                            3991. .9300
/rpt_family="Alu"
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12097. .12443
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family="Alu"
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1252. .11503
                                                                                                allele="A"
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Best Local Similarity 100.
Matches 244; Conservative
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-NOV-2003) Genetics, Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 5 (bases 1 to 191971)
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5 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (18-DEC-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
                                                                                                                                                                                                                                                                                   GGAGGAAGTGAGAAAGTTGGCACAGTCACGCCGGGCTTCGCAGGACCAGGTCACTCAGTG
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                                                                                                                                          1 AGCGCCGGGGGATTTAAATGCCACTAAAACGGTGATCCATCACTGCGGAAGCCGGCAAACT
                                                                                                                                                                                                                 TTGCAGGAGGCTCAGCCATTGGCTGACACCGTCACGTGCCCCTCCTCCAGCGTCCTCCG
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Center code: WUGSC
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On Nov 9, 2003 this sequence version replaced gi:33387055.
                                                                    Length 170237;
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Harkins,R. and Haakenson,W.
The sequence of Pan troglodytes BAC clone RP43-21L13
                                                                                                       Indels
                                                                    Score 242.4; DB 9;
Pred. No. 6.3e-60;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (01-AUG-2003) Genetics, Genome S
Forest Park Parkway, St. Louis, MO 63108,
4 (bases 1 to 191971)
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Contact: submissions@watson.wustl.edu
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/clone="RP43-169B4"
/clone_lib="RPCI-43"
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3 (bases 1 to 191971)
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2 (bases 1 to 191971)
                                                                    99.3%;
larity 99.6%;
Conservative
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                                                                                        Similarity
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                                                                        Query Match
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The RPCI-43 BAC Library has been constructed by Chung-Li Shu. DNA was isolated from white blood calls obtained from a male chimpanzee (Pan troglodytes, Clint', Yerkes #CQ471; birthdates = 6-6-80). The clone and detailed information can be obtained from ResGen (http://www.resgen.com) or Pieter de Jong and co-workers at
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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This sequence may not represent the entire insert of this
                                                                                                                                                            This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                             clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trigcaggaggercarragergacaccercacercecercercercercere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="Sequence derived from one plasmid subclone."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Sequence derived from one plasmid subclone."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 191971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Sequence derived from PCR product 156808. .156822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   derived from one plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Sequence derived from one plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from one plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is the entire insert of the clone.
Location/Qualifiers
1. .191971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.7%; Score 240.8; DB 9;
llarity 99.2%; Pred. No. 1.9e-59;
Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Pan troglodytes"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RPCI-43"
82205. .82239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nttp://www.bacpac.chori.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .157109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .160183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                     MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "map="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157072.
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241 ACAG 244

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ACCESSION

RESULT 4 AC129963

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VERSION KEYWORDS

SOURCE

REFERENCE

AUTHORS

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115406 GCCCTCCCGCCCCCCTCTTGCGCACTGTACATTCATATCTTTTTCTTCTCGGCCCCA 115465
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Rattus norvegicus, clone RP31-256A2, complete sequence.
ACLIEBEZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115286 AGCGCCGGGGATTTAAATGCCACTGAAAGGGTGATCCATCACCGCAGGAGCCAGCAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TTTGCAGGAGGCTCAGCCATTGGCTGAC-ACCGTCACGTGCCCCTCCTCCAGCGTCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 TGGAGGAAGTGAGAAAGTTGGCACAGTCACGCCGGGCTTCGCAGGACCAGGTCACTCAGT
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                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.9%; Score 204.8; DB 2; Length 128851; 92.2%; Pred. No. 6.1e-49; ive 0; Mismatches 18; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71201: gap of 100 bp
128851: contig of 57650 bp in length.
                                                                                                                                                                                                                                                                                                                        6913: contig of 6913 bp in length
7013: gap of 100 bp
10891: contig of 3878 bp in length
10991: gap of 100 bp
71101: contig of 60110 bp in length
71201: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .128851
/organism="Sus scrofa"
/mol_type="genomic DNA"
/db_xref="kaxon:9823"
/clone="RP44-485M13"
/clone_lib="RPCI-44 Male Porcine BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 112570)
Birren, B., Linton, L., Nusbaum, C. and
Rattus norvegicus, clone RP31-256A2
Center project Information
Center project name: L24464
Center clone name: 485_M_13
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1. .128851
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Best Local Similarity 92.2%
Matches 226; Conservative
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TITLE
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AC116662
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M. Submitted (16-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

B. Sirren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barran, N., Bastina, V., Bloom, T., Boquslavkiy, L., Boukbalter, B., Cooke, P., Dakacllano, K., Das, Z., S., Dodge, S., Farco, S., Farco, S., FitzGerald, M., Gage, D., Galagan, J., Chara, J., Malen, M., Hagos, B., Horton, L., Hulme, M., Iller, W., Major, J., Malen, S., Severy, P., Karatas, A., Kells, C., Madchan, L., Major, J., Malengan, J., Mouyen, C., Norman, C., Norman, C., Norman, C., Norman, J., Roy, A., Schauer, S., Schuube, R., March, M., Schauer, S., Schuube, R., March, M., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Sc
                                                                                                                                                            HTG 16-AUG-2002
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
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All repeats were identified using RepeatMasker:
                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                            AC129963.2 GI:22267860
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Sus scrofa (pig)
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Ali,A.,

Lander, E.

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Submitted Stabnassion

Burnert Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Burnen, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L., Characier, B., Brown, A., Campopiano, A., Chang, J., Characier, B., Campopiano, A., Chang, J., Characier, Cook, A., Cooke, P., DeArellano, K., Dear, K., Diaz, J.S., Dodge, S., Faro, S., Gorde, S., Gorder, M., Graham, L., Grand, P., Lones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehocaky, J., Levine, R., Marquis, N., Matchews, C., Macdonald, P., Major, J., Marquis, N., Matchews, C., Macdonald, P., Major, J., Marquis, N., Matchews, C., Macdonald, P., Major, J., Mardrim, J., Meneus, L., Nicol, R., Marphy, T., Volonnell, P., O'Neil, D., O'Neil, D., O'Liver, J., Petta, R., Pindara, M., Riley, R., Schauer, S., Schupback, R., Stange-Thomann, N., Stojanovic, N., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stanger, M., Travies, N., Trajilio, J., Vassillev, H., Vola, R., Wille, K., Travers, M., Travies, N., Trajilio, J., Vassillev, H., Viel, R., Wola, R., Shauer, S., Testaye, S., Theodore, J., Topham, K., Travers, M., Travies, N., Travers, N., Travers, N., Travers, N., Travers, N., Travers, N., Viel, R., Wola, R., Willer, Wola, R., Willer, Street, Cambridge, MA, Clatt, USA, All repeats were identified using Repeatmasker:

New Research, 320 Charles Street, Cambridge, MA, 02141, USA, Sait, A., Sait, A., Sait, A., Sait, L., A., Sait, L., A., Sait, L., A., Sait, L., A., Sait, L., A., Sait, L., A., Sait, L., A., Sait, L., A., Sait, L., A., Sait, L., A., Sait, L., L., Sait, R., Schauer, S., Schupback, L., Zimmer, A., and Zody, M., Vell, R., Wola, R., Wille, R., Schauer, J., Sawer, M., Sait, R., Schauer, S., Schupback, M., Sait, R., Schauer, S., Schupback, M., Sait, R., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S
Center: Whitehead Institute/ MIT Center for Genome Research
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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/clone lib="RPCI-31 Female Rat PAC"
480. .527
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2529__.256
/rpt_family="AT_rich"
4028__4050
/rpt_family="GC_rich"
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/db_xref="taxon:10116"
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Center clone name: 256_A_2
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Direct Submission
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complement (14299. .1421)
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8502. .18556
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1159. .21182
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27479. .27500
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42932. .42965
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

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Rattus norvegicus clone CH230-140P4, *** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGCGCCGGGGATTTAAATGCCACTAAAACGGTGATCCATCACTGCGGAAGCCGGCAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTGCAGGAGGCTCAGCCATTGGCTGACACGTCACGTGCCCCTCCTCCAGGGTCCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86607 fredeaddeddecheadcearraderaadaaareacaracaracarcaadacaraca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.6%; Score 199.2; DB 10; Length 112570;
88.5%; Pred. No. 2.6e-47;
iive 0; Mismatches 28; Indels 0; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                       /rpt_family="(TTCTCC)n"
57379. .67404
                                                                                     /rpt_family="(TTTTG)n"
60111. .60152
/rpt_family="G-rich"
62336. .62360
                                                                                                                                                                                                                                    /rpt_family="AT_rich"
58288. .68314
/rpt_family="(CA)n"
57106. .57145
/rpt_family="(CA)n"
58475. .58548
                                                                                                                                 /rpt_family="(CAA)n"
54373
                                                                                                                                                                                                                                                                                                                                                                         'rpt_family="C-rich"
'8618. .78664
                                                                                                                                                                                                                                                                                            rpt_family="G-rich"
1515. ,71616
                                                                                                                                                                                                                                                                                                                                       'rpt_family="(TG)n"
'2721. .72824
                                                                                                                                                                           note="Probably C."
                                                                                                                                                                                                                                                                                                                                                                                                'rpt_family="(TC)n"
'9428, 705--
                                                                                                                                                                                                                                                                                                                                                                                                                                              /9599. .79672
/rpt_family="(TC)n"
92718. .8274
                                                                                                                                                                                                                                                                                                                      rpt_family="(CA)n"
1778. .71825

    79511
    family="(GA)n"

                                                                                                                                                                                                                                                         'rpt_family="(T)n"
9226. .69282
                                                         family="Alus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="(T)n"
83175. .83210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC097087.12 GI:38044133
                                                                       .58636
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                                                           'rpt_fa
18595.
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Best Local Similarity
Matches 216; Conserv
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             repeat_region
                                            repeat region
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ORGANISM
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KEYWORDS
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ANTHORNA MATTON Natio. Part C. 24804).

AUTHORNA MATTON Natio. Part C. 24804).

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Bisaalo.K. Bait. J. Bait. J. Bait. Part Matton. M. Bait. Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton. Part Matton.
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-sacifold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                     Assembly programs. Atlas 3.0;

Consensus quality: 226791 bases at least Q40

Consensus quality: 2293471 bases at least Q30

Consensus quality: 229344 bases at least Q20

Estimated insert size: 240235; sum-of-contigs estimation

Estimates insert size: 274125; agarose-fp estimation
Quality coverage: 5x in Q20 bases; agarose-fp estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1005: contig of 1005 bp in length
3091: gap of 2086 bp
6209: contig of 1871 bp in length
6209: gap of 1247 bp
7864: contig of 1655 bp in length
8063: gap of 199 bp
18114: contig of 10051 bp in length
18226: gap of 112 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig of 201475 bp in length gap of unknown length contig of 1560 bp in length gap of 190 bp
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contig of 1403 bp in length
gap of unknown length
contig of 1221 bp in length
gap of unknown length
gap of unknown length
contig of 1389 bp in length
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contig of 1254 bp in length
gap of unknown length
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                                                                                                                                                                                      site: http://www.hgsc.bcm.tmc.edu/

    .234603
/organism="Rattus norvegicus"

                                                                                                                                              Center: Baylor College of Medicine
                                                                                                                                                                                                                                             Center project name: GIAV
Center clone name: CH230-140P4
                                                                                                                                                                                                       Contact: hgsc-help@bcm.tmc.edu
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clone_end:T?"
6210._.7864
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/note="wgs_end_extension
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/clone="CH230-140P4"
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gap of
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228063:
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In (Dases 1 to 29885)

Muzny, D.Marie., Metaker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Allen, C., Allen, H., Asbrooks, S., Amin, A., Anguiano, D.,
Banyalebechi, V., Aoyady, A., Ayodeji, M., Bards. E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barastead, M., Benahmed, F.,
Bryant, N., Bulary, C., Burch, P., Brown, M.,
Bryant, N., Bulary, C., Burch, P., Brown, M.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Durn, A., Durbin, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, R., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fraser, C.M., Gabisi, A., Gartia, A., Garner, M., Gerza, M.,
Gebregeorgis, E., Geer, K., Gall, R., Grady, M., Guerra, W., Guerra, W.,
Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
Harnandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hodges, M.,
Harnandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hohnson, R., Johnson, R.,
Jackson, L., Jacob, L., Jiang, H., Lebow, H., Lebow, H., Lebow, H., Lebow, H., Lebow, H., Lebow, H., Lebow, L., Li, Z., Liu, J.,
Liu, W., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
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Rattus norvegicus clone CH230-172C22, WORKING DRAFT SEQUENCE, 13
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25506 CCIGCCGCCCGCCTCTTGCGCACTGTACATTCATATCATTTTTCTTCTCTGGTCCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GGAGGAAGTGAGAAAGTTGGCACAGTCACGCCGGGCTTCGCAGGACCAGGTCACTCAGTG
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                      Query Match 81.6%; Score 199.2; DB 2 Best Local Similarity 88.5%; Pred. No. 2.6e-47; Matches 216; Conservative 0; Mismatches 28
                                                                                                                                         end sequence:BZ094084"
219802. .221361
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complement(8503. .923(
/note="clone_boundary
clone_end:T7
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
                                                                                                                                                                                                        /note="wgs contig"
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                                                                                                                 site: EcoRI
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                                   misc_feature
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AC122669
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KEYWORDS
SOURCE
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Jurect Submission
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:23265825.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold' individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that cones and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Magua, P., Martin, K., Martin, R., Martinez, E.,
Mangua, B., Magua, P., Martin, R., Martinez, E.,
Milosavijevic, A., Milosavijevic, M., Morris, K., Morris, K., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Nancelmen, O., Okulonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Plopper, F., Polndexter, A., Popovic, D., Primus, B., Pul, L.-L.,
Puazo, M., Quiroz, J., Rachlin, E., Reves, K., Regier, M.A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Rose, M., Rose, M., Rose, M., Rose, M., Rose, M., Rose, M., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Sanders, W., Savery, G., Scherer, S., Socotle, R., Sosa, J., Taylor, C.,
Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, M., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Walas, R., Wera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
Willson, R., Wullson, R., Walker, M., Yoon, L., Yoon, L., Yoon, V.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Weinstock, G. and Gibbs, R., Smith, D. R., Wilth, R., Smith, B., Millson, R., Milson, R., Weiss, R., Sutth, A., Smith, B., Milson, R., Weiss, R., Smith, D., Reinstock, G. and Gibbs, R., R., Millson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milson, R., Milso
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Direct Submission
Submitted (25-MXY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 298853)
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
* NOTE: This sequence may represent more than one clone.
* NOTE: This is a "working draft" sequence. It currently
* consists of 13 contigs. The true order of the pieces
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Contact: hgsc-help@bcm.tmc.edu
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                     13941: contig of 3941 bp in length
4041: gap of unknown length
18898: contig of 14857 bp in length
18898: contig of 10433 bp in length
18998: gap of unknown length
29531: gap of unknown length
20502: contig of 10433 bp in length
20502: contig of 10808 bp in length
77510: gap of unknown length
77510: gap of unknown length
17394: contig of 16808 bp in length
1394: contig of 1279 bp in length
2773: contig of 1279 bp in length
2873: gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 200633;
179517: contig of 13204 bp in length 179617: gap of 100 bp 200633: contig of 21016 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30; Indels
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HTG; HTGS PHASE1; HTGS FULLTOP; HTGS_ACTIVEFIN.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                /clone="RP23-329P9"
/clone_lib="RPCI-23 Female Mouse BAC"
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Mus musculus chromosome 6, clone RP23-103L13
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

75.4%; Score 184; DB 2;
Best Local Similarity 87.3%; Pred. No. 7.1e-43;
Matches 213; Conservative 0; Mismatches 30,
                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                                                        /mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="6"
                                                                                                    Location/Qualifiers
1. .200633
                                                                                                                                                                                                                                                                                                        /map="6"
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      166314
179518
179618
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TITLE
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AC091106
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                                            230512 cergécédecedeceretrigegeacreracianicararearritritritricregérectar 230571
                                                                                                                                                              AC015583 200633 bp DNA linear HTG 14-JAN-2002 Mus musculus chromosome 6 clone RP23-329P9 map 6, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                 GGAGGAAGTGAGAAAGTTGGCACAGTCACGCCGGGCTTCGCAGGACCAGGTCACTCAGTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 200633)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus chromosome 6, clone RP23-329P9
Unpublished
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Center: Whitehead Institute/ MIT Center for Genome Research
             NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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------- Project Information
Center project name: 11082
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11809: gap of 100 bp
51644: contig of 39835 bp in length
51744: gap of 100 bp
166213: contig of 114469 bp in length
166313: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Mus musculus (house mouse)
Mus musculus
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51745
166214
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153953

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153893

153834

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Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome
      'db_xref="taxon:10090"
                                                                                                            75.4%;
87.3%;
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                                                                                                           Query Match
Best Local Similarity 87.3
Matches 213; Conservative
                                  /map="6"
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AC123672
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TITLE
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                                                                  Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Treodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
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Center: Whitehead Institute/ MIT Center for Genome Research
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29735: contig of 5424 bp in length
29835: gap of 100 bp
44483: contig of 14648 bp in length
44883: gap of 100 bp
63467: gap of 100 bp
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75880: gap of 100 bp
143236: contig of 67356 bp in length
177955: gap of 100 bp
177955: gap of 100 bp
177955: gap of 100 bp
177955: gap of 100 bp
236214: contig of 58259 bp in length
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13553: gap of 100 bp
24211: contig of 10658 bp in length
24311: gap of 100 bp
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Center clone name: 103_L_13
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COMMENT

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Birren, B., Linton, L., Musbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukqalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Choagalo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gorette, M., Graham, L., Grand-Pierre, M., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacChean, C., McCarthy, M., McEwan, P., McKernan, K., Madrim, J., Maches, C., McCarthy, M., McEwan, P., McKernan, K., Madrim, J., Norbu, C., Norman, C.H., O'Conno, T., O'Donnell, P., O'Connell, P., O'Connell, P., O'Connell, P., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schuback, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, V., Strauss, N., Trayis, N., Trigilio, J., Tesfaye, S., Young, G., Zahnoun, J., Kobe, W., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zahnoun, J., Kabek, L., Zimmer, A. and Zody, M., Polieret, Submission, J., Lamer, R., and Zody, M., Polieret, Submission, J., Lamer, R., and Zody, M., Johnson, S., Severy, P., Lamar, A., Mylson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zahnoun, J., Zambek, L., Zimmer, A. and Zody, M., Johnson, S., Severy, P., Zahnoun, J., Submission, J., Zambek, L., Zimmer, A. and Zody, M., Wilson, S., Severy, P., Zahnoun, J., Ke, W., J., Jahner, S., Severy, P., Zahnoun, J., Tergilio, J., Tergilio, J., Tergilio, J., Tergilio, J., Tergilio, J., Tergilio, J., Young, G., Zahnoun, J., Zambek, L., Zahner, S., Severy, P., Zahnoun, J., Zahnoun, J., Zahnoun, J., Zahnoun, J., Zahnoun, J., Zahnoun, J., Zahnoun, J., Zahnoun, J., Zahnoun, J., Zahnoun, J., Zahnoun, J., Zahnoun, J., Zahnoun, J., Zahnoun, J., Zahnoun, J., Zahnoun, J., Zahnoun, J., Zahnoun, J., Zahnoun, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGGAAGTGAGAAAGTTGGCACAGTCACGCCGGGCTTCGCAGGACCAGGTCACTCAGTG 240
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                         Score 184; DB 2; Length 23
Pred. No. 7e-43;
0; Mismatches 30; Indels
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HTG; HTGS PHASE1; HTGS FULLTOP; HTGS ACTIVEFIN.
Mus musculus (house mouse)
                                                                                         /clone="RP23-103L13"
/clone_lib="RPCI-23 Female Mouse BAC"
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Mus musculus chromosome 6, clone RP23-253E11
chromosome="6"
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         Birch, S.C. Lander, Cambridge, Mr. 02111, 038.

Sharen, B. Nusbaum, C., Lander, E., Abouellell, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Frizderald, M., Gage, D., Galagan, J., Gardyna, S., Frizderald, M., Gage, D., Galagan, J., Gardyna, S., Hall, J., Houron, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., Machean, C., McCarthy, M., Macdonald, P., Mandor, J., Mathhews, C., McCarthy, M., Madori, P., Mandor, T., Manday, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Mador, T., Manday, V., Murphy, T., Naylor, J., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Spencer, B., Stange-Thomann, N., Schighovi, Stevery, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Travers, M., Talamas, J., Tesfaye, S., Thedore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wwan, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

Li Submitted (16-DEC-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Dec 16, 2003 this sequence version replaced gi:28975939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research
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Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Contact: sequence_submissions@genome.wi.mit.edu
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76471: gap of 100 bp
144414: contig of 67943 bp in length
144514: gap of 100 bp
169981: contig of 25467 bp in length
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178509: gap of 100 bp
236829: contig of 58320 bp in length.
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contig of 20809 bp in length
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13801: gap of 100 bp
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/clone lib="RPCI-23 Female Mouse BAC"
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/db_xref="taxon:10090"
/chromosome="6"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="teaxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
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Diagnosis of diseases associated with development genes
Patent: WO 0200927-A 128 03-JAN-2002;
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Length 236829;
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     DB 2;
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                                                   7e-43;
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Sequence 128 from Patent W00200927.
          Score 184;
Pred. No. 7
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Location/Qualifiers
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          Query Match
Best Local Similarity 87.3'
Matches 213; Conservative
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Strausberg, R.
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                                                                                                                                                                                                                                      AUTHORS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2529)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Morce, T., Wax, S.I., Wang, J., Haith, F.,

Biatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Hossak, S.A., McZwan, P.J.,

Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens homeo box Al, transcript variant 1, mRNA (cDNA clone MGC:45232 IMAGE:5537563), complete cds.
                                               01-FEB-2002
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                                                                                                                                                                                                                                                                                                                            /organism="synthetic construct"
/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AGGGCCGGGGATTTAAATGCCACTAAAACGGTGATCCATCACTGCGGAAGCCGGCAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4757 AGCGTCGGGGATTTTAAATGTTATTAAACGGTGATTTATTATTGCGGAAGTCGGTAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4817 TITGTAGGAGGITTAGTTATTGGTTGATATCGTTACGTGTTTTTTTTAGCGTTTTTTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                             PAT
                                                                                                                                                                                                              Olek,A., Piepenbrock,C. and Berlin,K. Diagnosis of diseases associated with development genes Patent: WO 2020927-A 127 03-JAN-2002; Epigenomics AG (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 6118;
                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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..4e-28;
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                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                             55.4%; Score 135.2; ilarity 72.1%; Pred. No. 1.4e Conservative 0; Mismatches
                                           AX344702
Sequence 127 from Patent WO0200927.
                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                 AX344702.1 GI:18492588
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synthetic construct
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Best Local &
RESULT 12
AX344702
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BC032547
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Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgcompgri.nih.gov/
Contact: nisc_mgcompgri.nih.gov/
Blakesley,R.W., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Grannite,S., Guan,X., Gupta,J., Haghighi,P.,
Dietrich,N.L., Grannite,S., Guan,X., Gupta,J., Haghighi,P.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,B.D.
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FQNRRMXQKKREKEGLLPISPATPPGNDEKAEESSEKSSSSPCVPSPGSSTSDTLTTS
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Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Fabey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y., Bouffard, G. G., Blakealey, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. W. Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Smailus, D. E., Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov series: IRAK Plate: 69 Row: k Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24497507. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 25, 2003 this sequence version replaced gi:21595838.
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                          human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/clone_lib="NIH MGC_72"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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/db_xref="GI:21595839"
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/db_xref="LocusID:3198"
/db_xref="MIM:142955"
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Best Local Similarity 89.23
Matches 58; Conservative
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                                                                                                                                       240 GACAG 244
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| db_xref="61:387146"
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PGPSYGLOGPDADVSGSYPPCAPAVYSGNLSTPWACHHHHHQTAGGTYGGSPGSBQTHHSY
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YGYVGQPNAVRTNFTTKQLTELBKEFHFNKYLTRARRVEIAASLQLNBTQVKIMFQNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein id="AAA37559.1"
db_xref="GI:309218"
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                                                                                                                                         ·.
                                                                                                                                                                                                                                                                                                                                                                                       MUSERAIA 12-JUN-1993 MRNA, complete cds, and alternate ERA-1-339 mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2216)
LaRosa,G.J. and Gudas,L.J.
Early retinoic acid-induced F9 teratocarcinoma stem cell gene ERA-1: alternate splicing creates transcripts for a Momeobox-containing protein and one lacking the homeobox Mol. Cell. Biol. 8 (9), 3906-3917 (1988)
                                                                                                                                                                           183 AGGAAGTGAGAAAGTTGGCACACAGTCACGCCGGGCTTCGCAGGACCAGGTCACTCAGTGAC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RMKÇKKREKEĞLLPISPĀTPPGSDEKTEESSEKSSPSPSAPSPAĞSTSDTLTTSH"
join(81. .422,626. .685)
/note="ERA-1-399 protein"
                                                                                                                                                                                                             1 AGGAAGTGAGAAAGTTGGCACAGTCACGCCGGGCTTCGCAGGACCAGGTCACTCAGTGAC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Original source text: Mouse (F9 teratocarcinoma stem cell line)
                                                                                                                                         Gaps
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                                                                                                Score 62; DB 9; Length 2529; Pred. No. 3.4e-07;
  759. .920
/note="homeobox; Region: Homeobox domain"
/db_xref="CDD:pfam00046"
                                                                                                                                       0; Indels
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/note="ERA-1-993 protein homeobox"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERA-1 protein; early retinoic acid protein.
Mus musculus (house mouse)
Mus musculus
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                                                                                                ch 25.4%; Score 62; DB 1 Similarity 100.0%; Pred. No. 3.4 62; Conservative 0; Mismatches
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/note="ERA-1-399 protein"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA, clone BRA-1-993.
Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Duboule,D.
                                                                                                                                                                                                                                                                                       1 TGGAGGAAGTGAGAAAGTTGGCACGGTCACCCAGGGCTTCGCAGGATCCAATCACTCAGT
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/db_xref="texon:10090"
/clone lib="library of H.Lehrach"
/dev_srage="embryo"
20. .435
/ene="Hox1.6"
/number=2
Pred. No. 8.6e-05;
                              89.2%; Pred. No.
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Compugen Ltd.
GenCore version (c) 1993 - 2004
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- nucleic search, using sw model OM nucleic

2004, 09:40:06; Search time 262.692 Seconds (without alignments) 3945.922 Million cell updates/sec September 18, Run on:

US-10-614-282-2 244 Perfect score:

1 agegeeggggatttaaatge......aecaggteaeteagtgaeag 244 IDENTITY NUC Scoring table: Sequence:

3373863 seqs, 2124099041 residues Searched:

Gapop 10.0 , Gapext 1.0

6747726 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 2000000000 Minimum

Maximum

Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002s:* N_Geneseq_29Jan04:* 1: geneseqn1980s:* 2: geneseqn1990s:* geneseqn2003as:* genesegn2003cs:* geneseqn2003bs:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:*

SUMMARIES

Description	Abn80111 Human che	Abn80110 Human che	Abl67703 Oesophagu		Adb62108 Human cDN		Aad49662 Mycobacte		Continuation (26 o	Continuation (26 o	Abl81906 Human ova	Adc87092 Human GPC		Adb62471 Human cDN	Adb62760 Human cDN		Human	Add14677 Human src	Adb49520 Primary r	Abl17819 Drosophil			Aax39667 Renal can
ID	ABN80111	ABN80110	ABL67703	AAA58471	ADB62108	AAL53730	AAD49662	ADC85996	AAI99682 25	AAI99683 ⁷ 25	ABL81906	ADC87092	ADA53147	ADB62471	ADB62760	ADB62119	ABA20479	ADD14677	ADB49520	ABL17819	ABL17828	ABL17818	AAX39667
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% Query Match		55.4	15.6	15.5	15.2	15.2	15.2	15.2	15.2	٠	14.8		14.6	14.6	14.6	•	•	•	14.5	14.3	14.3	14.3	14.2
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Aas76375 DNA encod	Abl63316 Breast ca	Acc00031 Human Bcr	Aas85030 DNA enccd	Aas76377 DNA encod	Aas85031 DNA encod	Abk83569 Human cDN	Abk83571 Human cDN	Aas18963 Wheat ace	Abs51803 Human mdd	Add29657 Human tum	Aad36071 Human adi	Aca64961 Human BCR	Adc86460 Human GPC	Ach03435 Genomic D	Abl27738 Drosophil	Aaf85371 Degenerat	Abx12105 Degenerat	Aaa50439 Porcine a	Aaa65527 Porcine B	Adb12722 Human pol	
AAS76375	ABL63316	ACC00031	AAS85030	AAS76377	AAS85031	ABK83569	ABK83571	AAS18963	ABS51803	ADD29657	AAD36071	ACA64961	ADC86460	ACH03435	ABL27738	AAF85371	ABX12105	AAA50439	AAA65527	ADB12722	AAQ76213
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14.2	14.2	14.2	14.2	14.2	14.2	14.1	13.9	13.8	13.7	13.7	13.7	13.5	13.4	13.4	13.4	13.3	13.3	13.3	13.3	13.3	13.3
34.6	34.6	34.6	34.6	34.6	34.6	34.4	34	33.6	33.4	33.4	33.4	33	32.8	32.8	32.6	32.4	32.4	32.4	32.4	32.4	32.4
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis; heart disease; epilepsy; histone deacetylation; muscular dystrophy; dwarfism; single nucleotide polymorphism; SNP; cytosine methylation; antidiabetic; cytostatic; articonvulsant; ds. Human chemically modified disease associated gene SEQ ID NO 128. BP. ABN80111/c ID ABN80111 standard; DNA; 6118 (first entry) 15-JUL-2002 ABN80111; RESULT 1

WO200200927-A2. Homo sapiens Synthetic.

03-JAN-2002

02-JUL-2001; 2001WO-EP007536.

2000DE-01032529. 2000DE-01043826. 30-JUN-2000; 01-SEP-2000;

(EPIG-) EPIGENOMICS AG.

Berlin K; Piepenbrock C, Olek A,

WPI; 2002-130908/17

Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes associated with development

Claim 1; SEQ ID NO 128; 27pp; English.

The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II) of genes associated with development selected from 87 genes listed in the specification such as ACCPN, ADFN, or AFDI and comprising one of 350 sequences (ABN79984-ABN80333) or their complements. The invention is useful for the diagnosis or therapy of diseases associated with

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1362 AACGCCGAAAATTTAAATACCACTAAAACGATAATCCATCATCACAAAGCGAAAACCGACAAACT 1303
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development genes, in particular disease related to homeobox containing genes (HOX), like diabetees, cancer, apoptosis related diseases, syndromes associated with congenital heart disease, epilepsy, diseases related to histone deacetylation, Currarino syndrome, diseases related with the development of the brain and limb girdle muscular dystrophy and dwarfism. Olisomers specific to each of the genes are useful for detecting the methylation state of all Cp6 dinucleotides within the 350 sequences or (II) and their complementary sequences, as primer oligonucleotides for the amplification of the 350 sequences, (II) and/or their complements and as oligomer probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs). Note: The sequence data for this patent did not form part of the printed specification but is based on patent did not form part of the printed specification but is based on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence information supplied to Derwent by the Buropean Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGCGCCGGGGATTTAAATGCCACTAAAACGGTGATCCATCACTGCGGAAGCCGGCAAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis; heart disease; epilepsy; histone deacetylation; muscular dystrophy; dwarfism; single nucleotide polymorphism; SNP; cytosine methylation; antidiabetic; cytostatic; anticonvulsant; ds.
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                                                                                                                                                                                                                                                                                                                                   Query Match

70.7%; Score 172.6; DB 6; Length 6118;
Best Local Similarity 81.9%; Pred. No. 3.6e-42;
Matches 199; Conservative 0; Mismatches 44; Indels 0;
                                                                                                                                                                                                                                                                                                Sequence 6118 BP; 1532 A; 235 C; 1646 G; 2705 T; 0 U; 0 Other;
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01-SEP-2000; 2000DE-01043826.
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The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II) cof genes associated with development selected from 87 genes listed in the specification such as ACCPN, ADFN, or AFD1 and comprising one of 350 concerts (ABN79984-ABN80333) or their complements. The invention is sequences (ABN79984-ABN80333) or their complements. The invention is development genes, in particular diseases associated with congenital heart disease, epilepsy, diseases related to histone deacetylation, Currarino syndrome, diseases related to histone deacetylation, Currarino syndrome, diseases related with the check of the prain and limb girdle muscular dystrophy and dwarfism. Conjugomers specific to each of the genes are useful for detecting the methylation state of all CPG dinucleotides within the 350 sequences or (II) and their complementary sequences, (II) and/or their complements and a solidomer probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNBs). Note: The sequence data for this single nucleotide polymorphisms (SNBs). Note: The sequence data for this content did not form part of the printed specification but is based on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4816
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                                    associated with development genes such as diabetes, comprises a sequence
of a segment of chemically pretreated DNA of genes associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CCCTCCCGCCCCCCTCTTGCGCACTGTACATTCATATCATTTTTCTTCTCCGGCCCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GGAGGAAGTGAGAAAGTTGGCACAGTCACGCCGGGCTTCGCAGGACCAGGTCACTCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4757 AGCGTCGGGGATTTAAATGTTATTAAACGGTGATTTATTATTGCGGAAGTCGGTAAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4817 TITGIAGGAGGITIAGITAITGGITGAIATCGITACGIGITITITITITIAGCGITITITCG
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               nucleic acid useful for diagnosis and therapy of diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.4%; Score 135.2; DB 6; ilarity 72.1%; Pred. No. 8.9e-31; Conservative 0; Mismatches 68;
                                                                                                                          Claim 1; SEQ ID NO 127; 27pp; English
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Matches 176; Conserv
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                                                                                      development
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WO200194629-A2.

WPI; 2002-130908/17.

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Gaps

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70; Indels

15.6%; Score 38; DB 6; Length 302250; 53.3%; Pred. No. 1.3; ive 0; Mismatches 70; Indels 0.

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         as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                          Sequence 302250 BP; 76116 A; 72066 C; 71554 G; 82514 T; 0 U; 0 Other;
                                                                                                                                                                                                151 ATTCATATCATTTTTCTTCTCCGGCCCCATGGAGGAAGTGAGAAAGTTGGCACACACTCACG
    as colon, breast, stomach, lung, thyroid, oesophageal,
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22-SEP-2000; 2000US-0234567P.
22-SEP-2000; 2000US-0234923P.
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25-SEP-2000; 2000US-023592P.
25-SEP-2000; 2000US-023592P.
25-SEP-2000; 2000US-0235982P.
25-SEP-2000; 2000US-023598P.
25-SEP-2000; 2000US-023598P.
27-SEP-2000; 2000US-0235638P.
27-SEP-2000; 2000US-0235638P.
27-SEP-2000; 2000US-0235638P.
27-SEP-2000; 2000US-0235638P.
27-SEP-2000; 2000US-0235638P.
28-SEP-2000; 2000US-0237863P.
29-SEP-2000; 2000US-0237173P.
02-OCT-2000; 2000US-0237294P.
02-OCT-2000; 2000US-0237294P.
03-OCT-2000; 2000US-0237294P.
03-OCT-2000; 2000US-0237294P.
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2000US-0234009P.
                                  30-MAY-2001; 2001WO-US010838
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05-JUN-2000;
18-SEP-2000;
18-SEP-2000;
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BLM gene cluster; bleomycin gene cluster; polyketide metabolite;
bleomycin; bleomycin analogue; holo-carrier protein; thiazolidine;
thiazoline; bithiazoline; microbial metabolite; sugar; ss.
                                        Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 8-30
                                                                                                                          /*tag= a
/transl except= (pos: 1. .3, aa: Met)
/note= "ORF 30; encodes AAB07556"
561. .2309
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/transl except= (pos: 1. .3, aa: Met)
/note= "ORF 29; encodes AAB07557"
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encodes AAB07559"
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23; encodes AAB07563"
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Horrigan

Endress G,

Ebner R,

Carter KC,

Augustus M, Weaver Z;

Soppet DR, Young PE,

WPI; 2002-188264/24.

(AVAL-) AVALON PHARM.

"ORF 22; encodes AAB07564"

The present invention describes a method (M1) for screening for an antinooplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABLG164 to ABLZ0101), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

Claim 1; SEQ ID NO 6040; 44pp; English

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chemically modifying biological molecules.
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P-PSDB; AAB07556, AAB07557, AAB07558, AAB07559, AAB07560, AAB07561, AAB07562, AAB07562, AAB07567, AAB07567, AAB07567, AAB07567, AAB07567, AAB07570, AAB07571, AAB07572, AAB07576, AAB07577, AAB07576, AAB07576, AAB07577, AAB07578.
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"ORF 14; encodes AAB07572"
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/note= "ORF 15; encodes AAB07571"
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53018. .54190
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                                    "ORF 21; encodes AAB07565
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/transl_excer_
/note= "ORF 20; e
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05-JAN-2000;
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Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27640 rcarecricos de de caraces de careces de caracece de caracedos de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de como de
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 goggaagccgccaaactritgcaggagctcagccarriggcrgacaccgrcacgrgccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 58857 BP; 7256 A; 25139 C; 19353 G; 7109 T; 0 U; 0 Other;
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Best Local Similarity 50.8%; Pred. No. 0.88;
Matches 90; Conservative 0; Mismatches 87; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Clone BRAWH20063010 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene cluster may also be used to produce sugars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cDNA encoding clone BRAWH20063010.
Claim 8; Page 97-136; 162pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1839, .2579
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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25-JAN-2002; 2002US-00350978
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us-10-614-282-2.rng

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The invention discloses a polymucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel

C polypeptides. Also claimed is a polypeptide encoded by the polymucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polymucleotide, immunologically assaying the polypeptide or peptide of the polymucleotide by contacting the polypeptide or peptide of peptide of the encoded protein, and observing the binding between the two, a transformant carrying the polymucleotide in an expressible manner and an antisense polymucleotide. The oligonucleotide is useful as a primer for synthesising the polymucleotide or as a probe for detecting the polymucleotide. The polymucleotide or as a probe of suspension are useful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and many disease-related competitions of genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell cranscription-related proteins, signal transduction-related proteins, cranscription-related proteins, as an encoding and activity and genes are involved in them can he need as enclated proteins are encoded proteins and proteins and proteins are encoded proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding them can be used as indicators for diseases (e.g. one special diseases, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a cDNA of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2087 Agdasacdacacrictrocrocrassacorocrocrocrocrocrocrocrassación 2146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148
                                                               useful for developing a diagnostic their expression and activity, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    data for this patent is not represented in the printed specification, bus is based on sequence information supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 CGGTGATCCATCACTGCGGAAGCCGGCAAACTTTTGCAGGAGGCTCAGCCATTGGCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Target RNA; target RNA:support-attached test compound; flow cytometry; mass spectrometry; high-throughput screening; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 ACCGTCACGTGCCCCTCCAGCGTCCTCCGCCCTCCCGCCCCCCCTTGCGCACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3050 BP; 491 A; 1023 C; 953 G; 583 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribonuclease P RNase P DNA SEQ ID No 24.
                                                               and polypeptides,
for regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAL53730 standard; DNA; 38110 BP.
                                                                                                                                              Claim 1; Page; 222pp; English
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                                                                                                         as targets of gene therapy
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                                                             New polynucleotides
  2003-450961/43
                                                                                   medicines
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                   P-PSDB; ADB64078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó:
                                                                                                                                                                                                                                                         Identifying a test compound that binds to a target RNA molecule by separating the detectably labeled target RNA:support-attached test compound complex from uncomplexed target RNA molecules and test compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               that binds to a target RNA molecule comprising separating the detectably labeled target RNA.support-attached test compound complex from uncomplexed target RNA molecules and test compounds. The separating process is carried out by flow cytometry and determining a structure of the type of test compound of the RNA.support-attached test compound complex by mass spectrometry. The method is useful for high-throughput screening of libraries of compounds to identify pharmaceutical leads.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gigantism; dwarfism; hypothyroidism; hyperthyroidism; cystic fibrosis; autoimmune disorder; aging; inflammation; diabetes; obesity; anorectic; neurodegenerative disorder; Parkinson's disease; gene therapy; virucide; haemostatic; antibacterial; nootropic; neuroprotective; cytostatic; fungicide; ribonuclease P; RNAase; enzyme; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel method for identifying a test compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amyloidosis, haemophilia; Alzheimer's disease; atherosclerosis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35959 céstresecrencarentarios de decentrador de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de desentación de des
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 CGGAAGCCGGCAAACTTTTGCAGGAGGCTCAGCCATTGGCTGACACCGTCACGTGCCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This polynucleotide sequence represents a DNA sequence related to detecting method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 38110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis ribonuclease P (RNAase) rnpB DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36079 GGCCGATCAGCGCAGGTTGCGAGTGCGGCACTTCGC 36115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 TCTTCTCCGGCCCCATGGAGGAAGTGAGAAGTTGGC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 7;
1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; Page 61-79; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD49662 standard; DNA; 38110 BP
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11-APR-2001; 2001US-0282966P
                                                                (PTCT-) PTC THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.2%;
52.2%;
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                                                                                                                                                                                            WPI; 2003-075534/07.
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                                                                                                                                                                                                                                                                                                                                                                by flow cytometry
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                                                                                                                                 Almstead NG;
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                                                                                                                                                                                                                                 library of test compounds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
tes 82; Conserv
                                                                                    WPI; 2003-075561/07
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                            Rando R,
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The invention relates to a novel polymucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polymucleotide of the invention may have a use in gene therapy. The polymucleotide and polympeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polymucleotide sequences shown in ADCRS548-ADCR7616 encode GPCR's of the
                                                                                                                                                                                                                                            New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
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Pred. No. 1.6;
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NAT INST ADVANCED IND SCI & TECHNOLOGY. CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
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                                                                                           Akiyama Y, Aburatani H;
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                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 449; 28pp; English.
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Best Local Similarity 64.7%;
Matches 55; Conservative
                                                                                                                                                          WPI; 2003-315783/31
                                                                                              Asai K,
                                                                                                                                                                                          P-PSDB; ADC85997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nvention
      (NAAD-)
(ADSC-)
                                                                                              Suwa M,
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                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for identifying a test compound that binds to a target RNA molecule, which comprises contacting a detectably labelled target RNA molecule with a library of test compounds under conditions that permit direct binding of the labelled target RNA to a member of the library of test compounds so that a detectably labeled target RNA.test compound complex is formed. The method is useful for sorceming libraries of compounds for those that are selectively bind to a pre-selected target RNA. The compounds are useful for inhibiting the formation of a specific bound RNA.host cell factor complexes in vivo. They are also useful for treating or preventing diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             overproduction or decreased protein function, such as amyloidosis, haemophilia, Alzheimer's disease, atherosclerosis, cancer, gigantism, dwarfism, hypothyroidism, hyperthyroidism, autoimmune disorders, aging, inflammation, cystic fibrosis, diabetes, obesity, neurodegenerative disorders, Parkinson's disease or infections (bacterial, viral, fungal). The invention is also used in gene therapy. The present sequence is Mycobacterium tuberculosis ribonuclease P (RNAse) rnpB DNA. This
                                                                                                                                                             Identifying a test compound that binds to a target RNA molecule for treating or preventing amyloidosis, hemophilia, cancer, gigantism, diabetes, by contacting a detectably labeled target RNA molecule with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence is used to illustrate the method of the invention
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                                                                                                                                                                                                                                                                                                                     Example; Page 70-88; 152pp; English
                                               Welch E;
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Gaps .. 155

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Continuation (26 of 45) of AA199682 from base 2500001 (Mycobacterium tuberculosis strai
WP Sequence split into 45 fragments LOCUS AA199682 Accession Aa199682
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2310000
2410000
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2910000
3010000
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910000
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AA199682_02
AA199682_03
AA199682_04
AA199682_05
AA199682_06
AA199682_07
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AAI99682_27
AAI99682_28
AAI99682_29
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AA199682_17
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGAAGCCGGCAAACTTTTGCAGGAGGCTCAGCCATTGGCTGACACCGTCACGTGCCCCT
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 TCTTCTCCGGCCCCATGGAGGAAGTGAGAAGTTGGC 201
                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                        Score 37;
Pred. No.
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                        3610000
3710000
3810000
3910000
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4110000
4210000
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52.2%;
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3600001
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                                                                                                                                                                                                                                                                                                                                                                            82; Conservative
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Pred. No. 1.9;
0; Mismatches 75; Indels 0
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API99683_00

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API99683_04

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Continuation (26 of 44) of AA199683
WP Sequence split into 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.2%;
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3700001
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AA199682 30
AA199682 31
AA199682 33
AA199682 34
AA199682 35
AA199682 36
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AA199682 41
AA199682 42
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AA199682 43
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Best Local (
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Sequence 1141 BP; 128 A; 440 C; 337 G; 236 T; 0 U; 0 Other;

invention

SXX

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The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and adolypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
              amount of polymucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovariant tumour protein comprising contacting T cells with (III) or (III) is useful in design and preparation of ribozyme molecules for inhibiting to isolate a full length gene from a suitable library egls; and library using well known techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GAIGITIGITGAAGAATAAGTGACTCCAIGCCCTTGAGAGTTGGTCAGAIGGGGAGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCTCAGCCATTGGCTGACACCGTCACGTGCCCTCCTCCAGCGTCCTCCGCCCTCCCGC 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 GATTIAAATGCCACTAAAACGGTGATCCATCACTGCGGAAGCCGGCAAACTTTTGCAGGA 69
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and thereby detecting ovarian cancer in the patient, where the
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 6; Length 374; Pred. No. 0.61;
                                                                                                                                                                                                                                                                                                                                              Sequence 374 BP; 69 A; 101 C; 104 G; 100 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75; Indels
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Local Similarity 51.9%;
nes 81; Conservative
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K, Irie R, Tamechika I;
                                                                                                                                                                              448
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                                                                                                                        29 CGGTGATCCATCACTGCGGAAGCCGGCAACTTTTGCAGGAGGCTCAGCCATTGGCTGAC
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Length 1141;
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Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
                                                            Indels
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   DB 9;
   14.6%; Score 35.6; DE 55.7%; Pred. No. 1.2;
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RES ASSOC BIOTECHNOLOGY.
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                                                                  Conservative
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Seki N, Yoshikawa T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
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     CGGTGATCCATCACTGCGGAAGCCGGCAAACTTTTGCAGGAGGCTCAGCCATTGGCTGAC
                                                     Human; ss; gene; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related protein; osteoporosis; neurological disease; cancer; tumour.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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2002US-00350978.
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Yoshikawa T,
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genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell regeneration. Membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins and genes encoding them can be used as indicators for diseases (e.g. osteopoxosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a cDNA of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.
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R, Tamechika I;
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Nio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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Pred. No. 1.6;
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Otsuka M,
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55.7%;
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2002US-00350978.
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J, Isono Y, H
Yoshikawa T, O
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marker or medicines for regulation of their expression and activity, or as targets of gene therapy

Claim 1; Page; 222pp; English

The invention discloses a polymuclectide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel consisted is a polympetide encoded by the polymuclectide or its partial peptide, an antibody binding to the polympetide or peptide or the polymuclectide, immunologically assaying the polympetide or peptide of the polymuclectide by contacting the polympetide or peptide of the polymuclectide by contacting the polympetide or peptide or peptide of the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polymuclectide in an expressible manner and an antisense polymuclectide. The oligonuclectide is useful as a primer for synthesising the polymuclectide, or as a probe of the control of the polymuclectides and encoded proteins are useful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and adiagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell regeneration. Membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins and genes cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a cDNA of the invention. Note: Some of the sequence cata for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.

Sequence 3089 BP; 496 A; 1043 C; 957 G; 593 T; 0 U; 0 Other;

Gaps 0; 14.6%; Score 35.6; DB 9; Length 3089; 55.7%; Pred. No. 1.6; 0. Mismatches 54; Indels 0; 68; Conservative Best Local Similarity Query Match Matches

2066 GGTCCTCCTCCTGCGGACCGCGCTCGGCCTGGGGACCGCGCCTCCTCCTCC 2125 148 29 CGGTGATCCATCACTGCGGAAGCCGGCAAACTTTTGCAGGAGGCTCAGCCATTGGCTGAC ŏ à pp

149 AC 150 ð

qq

2186 GC 2187

Search completed: September 18, 2004, 11:29:57 : 265.692 secs Job time us-10-614-282-2.rni

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                 Copyright
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OM nucleic - nucleic search, using sw model

September 18, 2004, 11:14:16; Search time 61.1263 Seconds (without alignments) 2215.217 Million cell updates/sec Run on:

US-10-614-282-2

l agcgccggggatttaaatgc.....accaggtcactcagtgacag 244 IDENTITY NUC Scoring table: Sequence:

Perfect score:

Gapop 10.0 , Gapext 1.0

682709 segs, 277475446 residues Searched:

1365418 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/ina/5A COWB.seg:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seg:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seg:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seg:*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seg:*
6: /cgn2_6/ptodata/2/ina/PCTUS COMB.seg:* Issued Patents NA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 2, Appli	Segmence 1. Appli	4	4		1		ì -	ì	ì ,-		` _	ì		2813		10	10	1221	6795	25, Ar	1404	Sequence 14130, A	_	14006,	6748,	
SUMMARIES	ID	US-09-103-840A-2	US-09-103-840A-1	US-08-232-463-14	US-08-934-386-4	US-09-712-529-6	US-08-458-568A-11	US-09-292-034-1	US-08-924-345-1	-053-	US-09-479-130-1	US-09-472-130A-1	US-08-916-421B-1	US-09-103-840A-2	US-09-103-840A-1	US-09-621-976-2813	US-09-345-217-3	US-08-870-126-10	US-09-445-247-10	US-09-252-991A-12219	US-09-252-991A-6795	-09	9-252	09-252-9	US-09-252-991A-6843	9	-09-252-9	US-09-252-991A-6876
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	Score	37	37	35.4	33.6	32.4	32.4	32.4		31	31	31	30.8	30.4	30.4	m	29.8	29.6	29.6	6	29	29	29	29	29	29	9	29
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Sequence 1871, Ap Sequence 1103, Ap Sequence 16, Appl		Sequence 19, Appl Sequence 1, Appl Sequence 19, Appl Sequence 2, Appli Sequence 1, Appli	173 102 102 23,
US-09-621-976-1871 US-09-016-434-1103 US-09-056-105-16	US-08-323-443B-1 US-09-144-085-3 US-09-105-537-32 US-09-105-537-5	US-09-320-878-19 US-09-141-908-1 US-09-657-440-19 US-08-658-136-2 US-08-658-136-1	US-09-489-039A-1736 US-09-620-3120-1027 US-09-620-3120-1026 US-08-306-691B-23 US-09-167-206-3 PCT-US93-062S1-78
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448 2861 3510	31571 33529 11220 36778	38506 38506 38506 53526	753 1227 1380 2301 2301 2301
11.8	11.8 11.8 11.7 11.7	11.7	11.6 11.6 11.6 11.6 11.6
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ALIGNMENTS

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104
                                                                                                             APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DAS EQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REPERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DAA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 CGGAAGCCGCCAAACTTTTGCAGGAGGCTCAGCCATTGGCTGACACGCGTCACGTGCCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 4403765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.2%; Score 37; DB 3;
52.2%; Pred. No. 0.6;
cive 0; Mismatches 79
                       ; Sequence 2, Application US/09103840A; Patent No. 6294328
                                                                                                APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 15.2
Best Local Similarity 52.2
Matches 82; Conservative
                                                                      GENERAL INFORMATION:
US-09-103-840A-2
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2520637 dégradecederchentendecedecedechaciantedecedecedecedecedenhacedes 2520696 2520697 CCACCAGCGACTCGGGCAATCCGGCGCCCGATCCGGGGCCCGGCCCAGGGTTCGCGGTG 2520756 CCTCCAGCGTCCTCCCCCCCCCCCCCTCTTGCGCACTGTACATTCATATT 164 2520757 CGCCGATCAGCGGCAGGTTGCGAGTGCGCACTTCGC 2520793 165 TCTTCTCCGGCCCCATGGAGGAAGTGAGAAGTTGGC 201 Sequence 1, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION: APPLICANT: FLEISCHMAN, RObert D.; APPLICANT: WHITE, OWEN R. US-09-103-840A-1 105 RESULT 2 Ωp ò d à

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42 CTGCGGAAGCCGGCAAACTTTTGCAGGAGGCTCAGCCATTGGCTGACACCGTCACGTGCC 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: Methods for Detecting Nucleic Acid
TITLE OF INVENTION: Segments Encoding Acetyl-CoA Carboxylase
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.8%; Score 33.6; DB 4; Length 1778; illarity 55.0%; Pred. No. 0.25; Conservative 0; Mismatches 54; Indels 0
                                                                                                                                                                                                                                                                 DB 1; Length 7218;
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COUNTRY: US
ZIP: 77210-4433
COMPUTER READBLE FORM:
MEDIUW TYPE: FIOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NDMABE: US/08/934,386
FILING DATE: 19-SEP-1997
CLASSIFICATION: 435
ATTONREY/AGENT INPORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
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REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,92
                                                                                                                                                                                                                                                                                              Pred. No. 0.12;
85; Mismatches
                                                                                                                                                                                                                                                                     14.5%; Score 35.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Arnold, White & Durkee P.O. Box 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08934386 Patent No. 6306636 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1172 YYYYYYYYYYYY 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 TICTICICGGCCCC 178
                                                                                                                                                                                                                                                                                                    6.78;
                            7218 base pairs
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 6.7%
Matches 9; Conservative
SEQUENCE CHARACTERISTICS:
                         LENGTH: 7218 base pai
TYPE: nucleic acid
STRANDEDNESS: single
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STRANDEDNESS: single
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Best Local Similarity :
....hes 66; Conservat
                                                                                                                 TOPOLOGY: linear | IMMEDIATE SOURCE: CLONE: pTZgpt-F1s
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STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                            APPLICANT: VENTER, John C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007, 00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 3; Length 4411529; Pred. No. 0.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 TCTTCTCCGGCCCCATGGAGGAAGTGAGAAGTTGGC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLFOX VIRUS NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE DOCKET NUMBER: 30472/114 IMMU FELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Foley & Lardner STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: VA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/23,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
APPLICATION NUMBER: EP 91 114 300.
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Mycobacterium tuberculosis CTHER INFORMATION: H37Rv US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-232-463-14; Sequence 14, Application US/08232463; Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INPORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 52.2%;
Matches 82; Conservative
      Claire M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (703)683-4109
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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      FRASER,
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LENGTH: 4411529
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
ANTI-SENSE: 1
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Sequence 11, Application US/08458568A
Patent No. 5821339
GENERAL INFORMATION:
APPLICANT: Schaffer, Priscilla A.
APPLICANT: Yeh, Lily
TITLE OF INVENTION: Infections and Methods for Treatment of Herpesvirus
TITLE OF INVENTION: Infections
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                          409 CACCCCCCACCTGCCCCACCTCCCTCCAACTCCTCCATGAATGCACGCATTTCAT 468
349 COGCCCAAGCAAGCAAGCAGGCCATGAGGACCAACTACCCGTCGTCCCCGTCTAGACCA 408
                                        102 CCTCCTCCAGGGTCCTCCGCCCTCCCGCCCCCTCTTGCGCCACTGTACATTCATATCAT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 IGRCAYTCYTCNCCYTCNCKNCCNARNGGNGTRCACATNCKNARNCCNCKNARCCANARN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 TABAACGGTGATCCATCACTGCGGAAGCCGGCAAACTTTTGCAGGAGGCTCAGCCATTGG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 SWDAINGCRCARCANGINCCNGCNCCRCAYIGNACRICNCKYICRCANGCNCCNGIDAIN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: This degenerate sequence encodes the amino acid CTHER INFORMATION: sequence of SEQ ID NO:5.

NAMMATKEX: misc feature
LOCATION: (1) ... (315)

OTHER INFORMATION: n = A,T,C or G
US-09-712-529-6
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13.3%; Score 32.4; DB 4; Length 315;
Best Local Similarity 33.6%; Pred. No. 0.3;
Matches 44; Conservative 22; Mismatches 65; Indels (
                                                                                                                                                                                                                                                    APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
APPLICANT: Mintmore, Theodore B.
APPLICANT: Whitmore, Theodore B.
APPLICANT: Thompson, Penny P.
TITLE OF INVENTION: Human Zven Proteins
FILE REFERENCE: 99-81
CURRENT APPLICATION NUMBER: US/09/712,529
CURRENT FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                          Sequence 6, Application US/09712529
Patent No. 6485938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WordPerfect 5.3
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 6
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CTCAGCCATTGGCTGACACGGTCACGTGCCCCTCCAGCGTCCTCCGCCCTCCCGCCC 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.3%; Score 32.4; DB 1; Length 12001; ilarity 64.9%; Pred. No. 1.5; Conservative 0; Mismatches 26; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 34094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Reddy, P. Seshidhar
APPLICANT: Tikoo, Suresh
APPLICANT: Tikoo, Suresh
APPLICANT: Babluk, Lozne
TITLE OF INVENTION: PORCINE ADENOVIRUS TYPE 3 GENOME
FILE REFERENCE: 293102002400
CURRENT APPLICATION NUMBER: US/09/292,034
CURRENT FILING DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32.4; DB 4;
Pred. No. 2.3;
0; Mismatches 91;
                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn R.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: DFCI-0029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3499
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Herpes simplex virus
STRAIN: Herpes Simplex Virus Type 1
US-08-458-568A-11
                 APPLICATION NUMBER: US/08/458,568A FILING DATE: 02-UUNE-1995 CLASSIFICATION: 435
                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,146
FILING DATE: 05-MAY-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Porcine Adenovirus Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-292-034-1/c; Sequence I, Application US/09292034; Patent No. 6492343; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.3%;
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                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 12001 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 CCCCTCTTGCGCAC 145
CURRENT APPLICATION DATA:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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STRANDEDNESS:
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COUNTRY:
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US-08-924-345-1
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3144 TCCCCGCACAGGCAGGCGTACTGCTGAGAGGTATCCGTCTCCATCTCGTCCGCCTCCGTA 3085
                                                                                                 3084 CACTGCAGCTGTAGTACATCTCACAGGTCTGATCGAAGCAGCAGGTCACACTCAGAC 3027
                                                  185 GAAGTGAGAAAGTTGGCACAGTCACGCCGGGCTTCGCAGGACCAGGTCACTCAGTGAC 242
                                                                                                                                                                                                US-08-924-345-1

Sequence 1, Application US/08924345

Patent No. 6224878

PAPLICANT: LEUNG-TACK Patricia
APPLICANT: LEUNG-TACK Patricia
APPLICANT: AUGONET Jean-Christophe, Francis
APPLICANT: AUGONET Jean-Christophe, Francis
APPLICANT: RIVIERE Michel, Emile, Albert
ITLE OF INVENTION: Mutants and vaccines of the Infectious
ITLE OF INVENTION: Bovine Rhinotracheitis virus
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Datemin Felease #1.0, Version #1.25 (EPO)
SOFTWARE: Patemin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Patemin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NATE:
APPLICATION NUMBER: US/08/924,345
FILING DATE: 09-ABP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/199,172
FILING DATE: 09-AUG-1994
APPLICATION NUMBER: 09-AUG-1994
APPLICATION NUMBER: BR 92 07930
FILING DATE: 26-UJN-1992
ATTORNEY/AGENT INFORMATION:
NAME: SARRO, THOMAS P.
REGISTRATION NUMBER: XI
TELEPHONE: (703) 92-7200
TELEPHONE: (703) 92-720
TELEPHONE: (703) 92-720
TELEPHONE: (703) 92-720
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TELEPHONE: (703) 92-720
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TELEPHONE: (704) 92-92-720
TELEPHONE: (704) 92-92-720
TELEPHONE: (704) 92-92-720
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NAME/KEY: CDS
LOCATION: 172..1311
COCHION: 172..1311
OTHER INFORMATION: /function= "envelope glycoprotein"
OTHER INFORMATION: /product= "glycoprotein gl"
OTHER INFORMATION: /standard_name= "BHV-1 gl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function= "envelop glycoprotein"
/product= "glycoprotein gE"
/standard_name= "BHV-1 gE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: LARSON AND TAYLOR
727 SOUTH TWENTY-THIRD STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Type 1 Bovine Herpesvirus STRAIN: ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4190 base pairs
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NAME/KEY: CDS
LOCATION: 1594..3318
OTHER INFORMATION: /Fus
OTHER INFORMATION: /prc
OTHER INFORMATION: /str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                42 CTGCGGAAGCCGGCAAACTTTTGCAGGAGGCTCAGCCATTGGCTGACACGTCACGTGCC 101
                                                                                                                                                                                                                                                                                                             102 CCTCCTCCAGCGTCCTCCGCCCTCCCCCCCCTCTTGCGCACTGTACATTCATATCAT 161
                                                                                                                                                                     Gaps
                                                                                                                                                                     .
                                                                                                              ch 13.1%; Score 32; DB 3; Length 4190; 1 Similarity 52.2%; Pred. No. 1.3; 71; Conservative 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09053866
; Patent No. 611075
; GENERAL INFORMATION:
; APPLICANT: Xu, Wenfeng
; APPLICANT: Yee, David P.
; TITLE OF INVENTION:
; TITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR
; TITLE OF INVENTION: PROTEASE.
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
LOCATION: 3388..3861
OTHER INFORMATION: /product= "protein US9"
OTHER INFORMATION: /standard_name= "BHV US9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                         3938 TTTTTCGGCACGCCC 3953
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              162 TITICITCICOGCCC 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Leith, Debra K
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 4895 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 176...1330 OTHER INFORMATION:
                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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NAME/KEY: misc feature
LOCATION: (84773)..(84773)
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US-08-916-421B-1
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            DB 3; Length 4895;
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                                                                         45; Indels
                                                                                                                                                                                                                                                    158 TCATTITICTICTCCGGCCCCATGGAGGAAGTGAGAAGTTGG 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31; DB 3
Pred. No. 2.9;
0; Mismatches
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0; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: Leith, Debra K
REGISTRATION NUMBER: 32,619
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TELECOMUNICATION INFORMATION:
TELEPHONE: 206-442-6674
TELEFAX: 206-442-6678
         12.7%;
56.3%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 4895 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                   58; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
Query Match
Best Local Similarity
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Best Local Similarity
Matches 58; Conserv
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US-09-479-130-1
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GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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3168 TCACTTTCTGTCAATGTCACCAGGGATAAGGTGGGGACAATGGG 3210
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                                                                                                           VES-09-472-130A-1

Sequence 1, Application US/09472130A

Sequence 1, Application US/09472130A

GENERAL INFORMATION:
APPLICANT: We senell, Scott R.
APPLICANT: Presnell, Scott R.
APPLICANT: Pester, David C.
ITLLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR PAR4
ITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR PAR4
ITLE OF INVENTION: (ZCHEMR2)
FILE REFERENCE: 98-100-01-07

CURRENT FILING DATE: 2000-01-07

PRIOR APPLICATION NUMBER: US/09/472,130A

CURRENT FILING DATE: 1998-04-01

NUMBER OF SEQ ID NOS: 21

SOFTWARE FEASESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.7%; Score 31; DB 4 56.3%; Pred. No. 2.9;
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OTHER INFORMATION: n equals a,
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LOCATION: (28222)
OTHER INFORMATION: n equals a,
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Best Local Similarity 56.39
Matches 58; Conservative
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; LOCATION: (176)...(1330)
US-09-472-130A-1
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LOCATION: (28257)..(282
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NAME/KEY: misc_feature
LOCATION: (68242)..(682442)
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NAME/KEY: misc_feature
LOCATION: (713622)..(713622)
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NAME/KEY: misc_feature
LOCATION: (741684)..(741684)
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NAME/KEY: misc_feature
LOCATION: (779455)..(779455)
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NAME/KEY: misc_feature
LOCATION: (779676)..(779676)
OCTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (855539)..(855539)
OCTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (816530)..(1084830)
OCTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (1084830)..(1084830)
OCTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (1086846)..(1096846)
OCTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (1086840)..(1096846)
OCTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (1108881)
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LOCATION: (1349491). (1349491)
OTHER INFORMATION: nequals a, t,
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LOCATION: (147091). (1470091)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (1569020). (1569020)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (1602912). (1602912)
OTHER INFORMATION: nequals a, t,
OTHER INFORMATION: nequals a, t, NAME/KEY: misc feature
LOCATION: (137081). (113081)
COTHER INPORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
OTHER INPORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t,
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OTHER INFORMATION: n equals a, t. NAME/KEY: misc_feature LOCATION: (1603734).(1603734) OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature LOCATION: (163798).(1637988) OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature NAME/KEY: misc_feature
LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (657203)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature

us-10-614-282-2.rni

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Search completed: September 18, 2004, 13:19:20
Job time : 83.1263 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                              2065396 GrccAdddccrcdccadcradgr
           CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                          12.5%;
50.7%;
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Best Local Similarity 9.6%; I
Matches 18; Conservative 99
                      NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
                                                                                                                                                                                                                            73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-621-976-2813/c
                                                                                                  TYPE: DNA
                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                                                                                                                             96 CGIGCCCTCCTCCAGCGICCTCCGCCCTCCCGCCCCCCCTTTGCGCCACTGTACAITCA
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FLEISCHWAN, Robert D.
APPLICANT: FLEISCHWAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 44366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
WUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WENTER, John C.
TILLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                           Length 1664976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.5%; Score 30.4; DB 3; Length 4403765; 50.7%; Pred. No. 64; Live 0; Mismatches 71; Indels 0;
                                                                                                               Indels
                                                                                                             32;
                                                                         DB 4;
                                                                                                           0; Mismatches
                                                                       12.6%; Score 30.8; 161.0%; Pred. No. 40;
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                      or
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                      ΰ
                                                                                                                                                                                                                     156 TATCATTTTTTTCTCCGGCCC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/09103840A; Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
// LOCATION: (1664854)..(1664855)
// OTHER INFORMATION: n equals a, t,
US-08-916-4218-1
                                                                   Query Match
Best Local Similarity 61.03
Matches 50; Conservative
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Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4403765
                                                                                                                                                                                                                                                                                                          RESULT 13
US-09-103-840A-2/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 ATTTAAATGCCACTAAAACGGTGATCCATCACTGCGGAAGCCGGCAAACTTTTGCAGGAG 70
                                                                                                                                                                                          88 CACCGICACGIGCCCCTCCAGCGICCTCCGCCCTCCCGCCCCCCCTTTGCGCACTG
                                                                                                                                                                                                                                                                                 148 TACATICATATCATTTTTTTTCTCCGGCCCCCATGGAGGAAGTGAGAAAGTTGGCACAGTC
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                                                                                                                                                      Gaps
                                                                                                   DB 3; Length 4411529;
                                                                                                                                                   ;0
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                                                                                                                                              71; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2813, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Unburs Milne Edwards, J.B.
APPLICANT: Johert, S.
APPLICANT: Gloradno, J.Y.
ITILE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75;
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                                                                                              Score 30.4; DB
Pred. No. 64;
0; Mismatches
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Pred. No. 2.8;
95; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           2065373
                                                                                                                                                                                                                                                                                                                                                                             208 ACGCCGGGCTTCGCAGGACCAGGT 231
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1
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GenCore version 5.1.6
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Copyright (c) 1993 - 2004 Compugen Ltd.	using sw model
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Run on: ĕ

September 18, 2004, 12:08:47; Search time 269.259 Seconds (without alignments) 4573.952 Million cell updates/sec US-10-614-282-2 Perfect score:

l agcgccggggatttaaatgc......accaggtcactcagtgacag 244 IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

3327077 seqs, 2523723180 residues Searched:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Minimum DB seq length: 0 Maximum DB seq length: 200000000

Published_Applications_NA:* Database

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		Segmence 2. Appli	Semilar 154 Am	Semience 116935	Semience 262 ann			Semience 333, App	Segrence 1889 An	Semience 1883, Ap	Segmence 1343, Ap	7 1 2	Semience 023, App	1 6	7	Seguence 316, App
		3 ID		./ US-10-614-282-2	US-09-962-832-154	3 US-10-424-599-116935	.6 US-10-104-047-262	.6 US-10-292-798-449	7 US-10-322-281-359	US-09-867-701-4884	.5 US-10-017-161-1889	.6 US-10-292-798-1545	6 US-10-094-749-715	6 US-10-104-047-625	6 US-10-104-047-914	5 TIS-10-104-047-27	27 - 17 - 17 - 17 - 17 - 17 - 17 - 17 -	./ US-IO-//5-169-316
		Match Length DB	1 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	T 557	302250 9	288 1	3050 1	63155 1	89829 1	374 9	1141 1	1141 1	2179 1	2818 1	3089	3743 1	1 11000	348/3 T
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		Score	1 5	117	38	37.2	37.2	37	36.2	36	35.6	35.6	35.6	35.6	35.6	35.6	2 20	0.00
	Result	No.	; ; ; ; ;	4	0	о С	4	Ŋ	9 U	7	80	6	10	11	12	13	7.7	+

Sequence 141831, Sequence 78180, A	quence 58	198	530 e 530	530	Sequence 5305, Ap	equence 273	25,	equence 8,		Sequence 153404,	(a)	Seguence 26175, A	44508,	4	Sequence 913, App	'n	H		9	9	9	596	e 1522.	a	e 30970,
US-10-424-599-141831 US-10-437-963-78180 US-10-437-963-78180	09-954-531-586 -10-193-651-22	7-192-1-692-53	8-10-040-862-53	10-057-475B-530	-10-154-884B-53 -10-764-324-530	14-27	-10-466-164-2	-09-957-956-8	10-027-632-1	-10-027-632-1	-10-767-701	-10-437-963-2	10-369-493-4	-10-437-963-	-10-292-798-91	-09-844-	-10-424-599-1	-10-	-10-212-201-	-10-680-755A-	10-680-800A-	-10-424-599-59	-10-260-238-15	10-369-493-2	-493-30
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ALIGNMENTS

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Sequence 2, Application US/10614282
| Sequence 2, Application US/10614282
| Publication No. US20040082034A1
| GENERAL INFORMATION:
| APPLICANT: LEE, DUNG-FANG
| APPLICANT: LEE, DUNG-FANG
| TITLE OF INVENTION: INTERNAL RIBOSOME ENTRY SITE OF THE LABIAL GENE FOR TITLE OF INVENTION: PROTEIN EXPRESSION
| FILE REFERENCE: 08842.0001-00000
| CURRENT APPLICATION NUMBER: US/10/614,282
| PRIOR APPLICATION NUMBER: 60/394,270
| PRIOR APPLICATION NUMBER: 60/394,270
| RIGHER OF SEQ ID NOS: 2
| SOFTWARE: PATENTIN Ver. 2.1
| SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TITGCAGGAGGCTCAGCCATTGGCTGACACCGTCACGTGCCCCCTCCTCCAGGGTCCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGCGCCGGGGATTTAAATGCCACTAAAACGGTGATCCATCACTGCGGAAGCCGGCAAACT
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100.0%; Pred. No. 5.5e-75;
live 0; Mismatches 0;
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Best Local Similarity 100.
Matches 244; Conservative
                                                                                                                                                                                                                                                                                                                                           TYPE: DNA

ORGANISM: Homo sapiens

US-10-614-282-2
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US-10-614-282-2
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US-10-292-798-449

Sequence 449, Application US/10292798

Sequence 449, Application No US20030235833A1

Sequence 449, Application No US20030235833A1

Sequence 449, Application No US2003023583A1

APPLICANT: WINA, MAXIMA

APPLICANT: ASAI, KIYOSHI

APPLICANT: ABURALAMI, HIROYUKI

APPLICANT: ABURALAMI, HIROYUKI

APPLICANT: ABURALAMI, HIROYUKI

TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS

FILE REFERENCE: 084335/166

CURRENT APPLICATION NUMBER: US/10/292,798

CURRENT FILING DATE: 2002-11-13

FRIOR FILING DATE: 2001-12-18
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                                                                                                                                                                                                                                                59 CITITGCAGGAGGCICAGCCATTGGCTGACACCGTCACGTGCCCCTCCTCCAGCGTCCTC 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 CGGTGATCCATCACTGCGGAAGCCGGCAAACTTTTGCAGGAGGCTCAGCCATTGGCTGAC
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                                                                                                                   Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence 262, Application US/10104047
; Sequence 262, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA; FILE SPERRENCE: HI-AG105;
; CURRENT APPLICATION NUMBER:
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                               Score 37.2; DB 13;
Pred. No. 0.014;
0; Mismatches 55;
                 OTHER INFORMATION: Clone ID: PAT_MRT3847_76603C.1 US-10-424-599-116935
                                                                                                                          15.2%;
54.5%;
                                                                                                                                                                                            Conservative
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                                                                                                                          Query Match
Best Local Similarity
Matches 66; Conserv
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LENGTH: 3050
FEATURE:
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US-10-424-599-116935/A

J Sequence 116935, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Kovalic David K

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF SERENCE: 38-21(53223)B

CURRENT APPLICATION UNMERS: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 116935

LENGTH: 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARENT NO. USZUGZOLIUGZIAI
APPLICANT: Boner, Reinhard
APPLICANT: Ebner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-74
CURRENT APPLICATION NUMBER: US/60/235,077
PRIOR APPLICATION NUMBER: US/60/235,077
PRIOR PILING DATE: 2000-09-25
PRIOR PILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 259
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.0
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                                  GGAGGAAGTGAGAAAGTTGGCACAGTCACGCCGGGCTTCGCAGGACCAAGGTCACTCAGTG 240
                                                                         151 ATTCATATCATTTTTTTTTTTCTCCGGCCCCCATGGAGGAGGTGAGAAGTTGGCACAGTCACG
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Pred. No. 0.067;
0; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294525 ATTGGCATGGCCTGGGCAGGGACATGTGTG 294496
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LOCATION: (1)...(288)
OTHER INFORMATION: unsure at all n locations
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 154, Application US/09962832 Patent No. US20020110821A1
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Local Similarity 53.3%;
les 80; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                       241 ACAG 244
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US-09-962-832-154/c
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SEQ ID NO 154
THNGTH: 302250
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96 CGIGCCCCTCCAGCGICCTCCGCCCTCCCCCCCCCCTTGGGGCACTGTACATTCA 155 0; Gaps Sequence 359, Application US/10322281
| Publication No US20040126762A1
| Publication No US20040126762A1
| GENERAL INFORMATION:
| APPLICANT: David W. Morris
| APPLICANT: Marc S. Malandro
| TITLE OF INVENTION: Novel Compositions and Methods in Cancer:
| TITLE OF INVENTION: Novel Compositions and Methods in Cancer:
| CURRENT APPLICATION WURBER: US/10/322,281
| CURRENT FILING DATE: 2002-12-17
| NUMBER OF SEQ ID NOS: 866
| SOFTWARE: FastSEQ for Windows Version 4.0
| LENGTH: 89829 Query Match
15.2%; Score 37; DB 16; Length 63155;
Best Local Similarity 64.7%; Pred. No. 0.091;
Matches 55; Conservative 0; Mismatches 30; Indels 0 NAME/KEY: modified base LOCATION: (57166)...(57168) OTHER INFORMATION: a, t, c, g, unknown or other NAME/KEY: modified base LOCATION: (57182). [57186) OTHER INFORMATION: a, t, c, g, unknown or other DEACHINE MODIFIED DASE
LOCATION: (57188)...(57191)
OTHER INFORMATION: a, t, c, g, unknown or other DECENTION: (57223). (57322)
OTHER INFORMATION: a, t, c, g, unknown or other ; LOCATION: (60650). (60749); OTHER INFORMATION: a, t, c, g, unknown or other US-10-292-798-449 g, unknown or other FEATURE:
NAME/KEY: modified_base
LOCATION: (57198)..(57198)
OTHER_INFORMATION: a, t, c, g, unknown or other or other g, unknown or other 60911 İciciririnininini 156 TATCATTTTCTCCGGCCCCAT 180 g, unknown NAME/KEY: misc_feature LOCATION: (1)...(89829) OTHER INFORMATION: n = A,T,C or G US-10-322-881-359 NAME/KEY: modified base LOCATION: (57179)...(57180) OTHER INFORMATION: a, t, c, NAME/KEY: modified base LOCATION: (59045)...(59144) OTHER INFORMATION: a, t, c, LOCATION: (57175)...(57175)
OTHER INFORMATION: a, t, c, NAME/KEY: modified_base NAME/KEY: modified_base TYPE: DNA ORGANISM: Mus musculus RESULT 6 US-10-322-281-359/c P g Š ð

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Query Match
Best Local Similarity 55.7%;
Matches 68; Conservative
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US-10-292-798-1545
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ORGANISM: Homo sapiens
                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (201)..(941)
US-10-017-161-1889
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                                                                    NAME/KEY: SOURCE
LOCATION: (1)..(1141)
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Best Local Similarity
Matches 68; Conserv
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US-10-292-798-1545
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NAME/KEY: CDS
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SEQ ID NO 1545
LENGTH: 1141
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LENGTH: 1141
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                                                                                                                                                117 rececercedecececererrececentraterraterraterraterretrecent 176
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                                                                           Gaps
Score 36.2; DB 17; Length 89829;
Pred. No. 0.19;
0; Mismatches 53; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                             PACIENT NO. USES CONTRAINED AND APPLICANT: AGIACL, Paul A. APPLICANT: AGIACL, Paul A. APPLICANT: Jones, Robert APPLICANT: Jones, Robert APPLICANT: Harlocker, Susan L. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.497

CURRENT FILING DATE: 2001-05-29

NUMBER OF SEQ ID NOS: 10912

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.8%; Score 36; DB 9; Length 374; 51.9%; Pred. No. 0.039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SUMMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ARIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE REPERENCE: 084335/0152
FILE REPERENCE: 084335/0152
CURRENT FILING DATE: 2002-12-18
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
NUMBER: OF SEQ ID NOS: 2430
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cccaccccrcrasgccrcaaggggcrcarcrrrr 276
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Publication No. US20030143668A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 Sequence 4884, Application US/09867701 Patent No. US20020132237A1
   14.8%;
56.2%;
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                                       68; Conservative
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US-09-867-701-4884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
   Query Match
Best Local Similarity
Matches 68; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 4884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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Score 35.6; DB 15;
Pred. No. 0.077;
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TITLE OF INVENTION: NO. US20030236392Alel full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
FRIOR APPLICATION NUMBER:
FRICH FILING DATE: NUMBER:
NUMBER OF SEQ ID NOS: 4096
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Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR PELLING DATE:
PRIOR FILING DATE:
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Pred. No. 0.1;
0; Mismatches 54;
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Matches 68; Conservative
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SOFTWARE: Patentin Ver. 2
SEQ ID NO 625
LINGTH: 2818
TYPE: DNA
ORGANISM: HOMO sapiens
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CRGANISM: Homo sapiens
US-10-104-047-914
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US-10-104-047-273
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Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELLY RESEARCH INSTITUTE
APPLICANT: HELLY RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
FILE REPERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
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CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: UP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver: 2.1
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APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YUUKO
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SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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Matches 68; Conservative
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OTSUKA, KAORU
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IRIE, RYOTARO
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                         Publication No. US20 GENERAL INFORMATION:
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US-10-094-749-715
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US-10-094-749-715
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| Publication No. US20040175743A1
| Publication No. US20040175743A1
| GENERAL INFORMATION:
| APPLICANT: Wyeth
| APPLICANT: Twine, Natalie
| APPLICANT: Trepicchio, William
| TITLE OF INVENTION: Mathod for Monitoring Drug Activities In Vivo
| FILE REFERENCE: AMAIO1800 (031896-013000)
| CURRENT APPLICATION NUMBER: US/10/775,169
| CURRENT PILING DATE: 2004-02-11
| NUMBER OF SEQ ID NOS: 5278
| SOFTWARE: PatentIn version 3.2
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Pred. No. 0.11;
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55.7%;
                                           SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 273
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NUMBER OF SEQ ID NOS: 4096
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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APPLICANT: La Rosa Thomas J APPLICANT: Kovalic David K APPLICANT: Zhou Yihua APPLICANT: Cao Yongwei

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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERENCE: 38-21(5323) B CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 141831
LENGTH: 900
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14.5%; Score 35.4; DB 13;
Best Local Similarity 57.8%; Pred. No. 0.084;
Matches 63; Conservative 0; Mismatches 46;
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US-10-424-599-141831
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BE649209 UI-M-BH2.
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AK083575 Mus muscu
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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/ dev stage="15.7.3 days"
/ dev stage="15.7.3 days"
/ dev stage="15.7.3 days"
/ dev stage="15.7.3 days"
/ lab host="UI-M-BH10B (life Technologies)"
/ clone lib="NH10B (life Technologies)"
/ clone lib="NH1 BMAP M $3.3"
/ note=="Vector: pT713D-Fac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Bco R1; The NIH BMAP M $3.3 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus) after a series of subtractions to reduce the representation of conks from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH BMAP M $3.3. NIH BMAP M $3.1 NIH BMAP M $3.1 NIH BMAP M $3.2 INH BMAP M $3.2 clones from which 3' ESTs had been derived was used as driver in a hybridization with the NIH BMAP M $2. library in the form of single-stranded circles. The remaining and the form of single-stranded circles. The remaining circles and the subtraction stranded circles. The remaining circles and the subtraction with the NIH BMAP M $2. library in the form of single-stranded circles. The remaining circles and single-stranded circles. The remaining circles and single-stranded circles. The remaining circles and single-stranded circles. The remaining circles and single-stranded circles. The remaining circles and single-stranded circles. The remaining circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles and circles an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to
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Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The following repetitive elements were found in this cDNA sequence: 356-388, >GC_rich#Low_complexity
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 343)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCGCCGGGGATTTAAATGCCACTAAAACGGTGATCCATCACTGCGGAAGCCGGCAAACT
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/strain="C57BL/6J"
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/dab host="DH10B (Life Technologies)"
/clone lib="NIH BMAP M S.3."
/note="vector: pT713D-Pac (Pharmacia) with a modified
polylinker; Site l: Not I; Site 2: Eco RI; The
NIH BMAP M S3.3 library is a subtracted library of a
series, ultimately derived from a mixture of individually
tagged normalized libraries from ten regions of the mouse
brain (cerebellum, brain stems, olfactory bulbs,
hypothalamus, orttex, amygdala, basal ganglia, pineal
gland, striatum, hipoccampus) after a series of
subtractions to reduce the representation of cDNAs from
which ESTs had already been generated. The following
serially subtracted libraries were generated in this
process: NIH BMAP M S3.3 NIH BMAP M S2.
The subtracted libraries were generated in this
stollows: PCRamplified cDNA inserts from NIH BMAP M S2.
clones from which 3' ESTs had been derived was used as
a follows: PCRamplified cDNA inserts from NIH BMAP M S2 ilbrary
in the form of single-stranded circles (subtracted library) was purified
by hydroxypapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (LifeTechnologies) to generate the
NHH BMAP M S3.3 library. This procedure has been
previously described (Bonaldo, Lennon and Soares, Genome
Research 6:791806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                               Oligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. CDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP CDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP CDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence: 13-50, SGC rich#Low complexity
DOLYA-NO.
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Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                    National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
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85.3%; Pred. No. 1.7e-21;
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                                                                                                Genome Res. 6 (9), 791-806 (1996)
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                        Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
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Best Local Similarity
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 625)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
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Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
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/cell_type="Epithelial"
/cell_line="SNU-601"
/lab_host="Top10F'"
/clone_lib="S9SNU601"
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/sex="M"
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Plate: 73 row: G column: 08
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/db xref="taxon:9606"
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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AKO83575 20-SEF MRNA linear HTC 20-SEF Mus musculus 9 days embryo whole body CDNA, RIKEN full-length enriched library, clone:D030047C07 product:homeo box Al, full
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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6 (9), 807-828 (1996)
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BB655265.1 GI:16489093
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Best Local Similarity lvv..

Rest rocal 77; Conservative
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Eukaryota, Metazoa,
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  Res.
                       97044478
8889549
     Genome
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VERSION
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AUTHORS
                       MEDLINE
PUBMED
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BB655265
  JOURNAL
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                                                                                                                                                                                                                                                                                                                            /db_xref="FANTOM DB:D030047C07"
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/clone="Whole body"
/clone="Tib="RIKEN full-length enriched mouse cDNA library"
/dev stage="9 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA199907
zg52a07.rl Stratagene neuroepithelium (#937231) Homo sapiens CDNA clone IMAGE:645204 5' similar to TR:G1195540 G1195540 HOXA1
{ALTERNATIVELY SPLICED} . ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \(\frac{\codon start=1}{\documents \text{ start=1}}\)
\(\fracterin id=\text{ id=0.8A038956.1"}\)
\(\fracterin id=\text{ id=0.1506039 \text{ }"}\)
\(\frac{\document \text{ id=0.1506039 \text{ }"}{\text{ ranslation=\text{ imNNARMNSFLEYPILGSGDSGTCSARAYPSDHGITTFQSCAVSA}}\)
\(\text{ NSCGGDDRFLVGRGVQ1SSPHHHHHHHHHPQTATYQTSGNLG1SYSHSSCGPSYGA}\)
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IHHSYGGBQQTLALATYNNSL.SPLHASHQEACRSPASETSSPAQTFDWMKVKRNPPKT
GKYGEYGYVGQPNAVRTNFNTKQLTELEKEFHFNKYLTRARRVEIAASLQLNETQVKI
WFQNRRMKQKKREKEGLLPISPATPPGSDEXTEESSEKSSPSPSAPASFASSTSDTLTT
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Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, S., Soares, M.B., Tan, F., Thierry-Meg, J.,
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 ACATICATATCATTTTCTTCTCCGGCCCCATGGAGGAAGTGAGAAGTTGGCACAGTCA 208
                       cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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Generation and analysis of 280,000 human expressed sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="unnamed protein product; homeo box Al
(MGD|MGI:91170, GB|NM_010449, evidence: BLASIN, 99%
match=2216)
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                                                                                                                                                Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 CGCCGGGCTTCGCAGGACCAGGTCACTCAGTGACAG 244
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/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA199907
AA199907.1 GI:1795641
                                                                                                                                   prepare mouse tissues.
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AA199907
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/Glome="IMAGE:645204"
/dev_stage="Ntera-2/RA neuroepithelial cells"
/dev_stage="Ntera-2/RA neuroepithelial cells"
/dab_host="SQLR (kanamycin resistant)" (#937231)"
/clone_lib="Stratagene neuroepithelium (#937231)"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
Xhol; Cloned unidirectionally. Primer: Oligo dT. NT2
cells (Ntera-2/Gt.D1) induced with Retinoic Acid for 24
hours. Average insert size: 1.5 kb; Uni-ZAP XR Vector; ~5'
adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 TCTCCGGCCCCATGGAGGAAGTGAGAAGTTGGCACAGTCACGCCGGGCTTCGCAGGACC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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BB655265 RIKEN full-length enriched, 9 days embryo Mus musculus cDNA clone D030047C07 5', mRNA sequence.
                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Final: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 195.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 428;
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2.5e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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Mus musculus (house mouse)
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Composer. Titoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. Sugahara, Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bmail: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayateu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
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                                                                            Akimura, T., Caraninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K.,
Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K.,
Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Komno, H., Kouda, M.,
Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N.,
Sagabe, Y., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Tanaka, T., Tomaru, A., Toya, T., Watahiki, R., Yasunishi, R.,
Muramatsu, M. and Hayaahizaki, Y.,
RIKEN Bncyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
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/lab_host="SOLR"
                                                      Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e mouse tissues.
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BB846631 RIKEN full-length enriched, adult male kidney Mus musculus
EDB46631
                                                                                                                                                                                                                                                                                                                                                                                 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-171 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itch,W., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
Wagi,K., Fujiwake,S., Inoue,K., Toawa,M., Chara,E., Watshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 ATTCATATCATTTTTCTTCTCCGGCCCCCATGGAGGAGGTGAGAAGTTGGCACAGTCACG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="RIKEN full-length enriched, 9 days embryo" /note="Site 1: Sal1; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki, Y. Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   caggetricgcargarccaarcacrcagrgacag 94
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="D030047C07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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88.3%;
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Best Local Similarity
Matches 83; Conserva
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source

FEATURES

ORIGIN

BB846631.1 GI:17085006

/ERSION

DEFINITION ACCESSION

RESULT 7 BB846631

61

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ORIGIN

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/cell_type="teratocarcinoma"
/cell_line="NT2"
/coll_line="NT2"
/clone_lib="rypep2"
/note="Vector: PME18SFL3; mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"
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                                                                                                                                                                                                                                              Contact: Takao Isogai
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3375
Fax: 81-438-52-3386
Fax: 81-438-52-3986
Fax: Brail: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; CNNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                   1 (bases 1 to 851)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AU132057 AU2RP3 Homo sapiens CDNA Clone NT2RP3003711 5', mRNA
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
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2.1e-05;
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ilarity 100.0%; Pred. No. 2.1
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP2002264"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
    AU127876
AU127876.1 GI:10988230
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AU132057.1 GI:10992411
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HRI human cDNA project
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Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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                                                           Homo sapiens (human)
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AGENCOURT_6447587 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5537563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llh.gov
Plate: LLAM12229 row: a column: 20
High quality sequence stop: 717.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1104)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                       62
                                                                                                                       Gaps
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                                             Gaps
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    Length 432;
                                           10; Indels
    Score 73; DB 10;
Pred. No. 2.7e-08;
                                         0; Mismatches
                                                                                                                                                            216 CTTCGCAGGACCAGGTCACTCAGTGACAG 244
                                                                                                                                                                                                   63 cricecaegarccaarcacreagreacae 91
                                                                                                                                                                                                                                                                                                                                                                                BM462913.1 GI:18511953
    29.9%;
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                         5', mRNA Sequence.
BM462913
                                         79; Conservative
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RESULT 11

AA070261

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED

COMMENT

FEATURES

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/cell type="teratocarcinoma"
/cell_line="NT2"
/clone_lib="NT2R2"
/clone_lib="Vector: phE18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"
     Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 640)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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                                                                                                                                                                                                                                                                                                                                 22.1%; Score 54; DB 100.0%; Pred. No. 0.0; ive 0; Mismatches
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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Best Local Similarity 100.0
Matches 54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pME183FL3; mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"
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1 (bases 1 to 471)
1 (bases 1 to 471)
1 (bases 1 to 471)
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, M., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schelemberg, K., Soares, M. B., Tan, F., Thierry-Meg, J., Travsakis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
Marning: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should kept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA070261 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530888 5' similar to SW:HXAl_MOUSE P09022 HOMEOBOX PROTEIN HOX-Al ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                           Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
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Location/Qualifiers
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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100.0%; Pred. No. 0.0013;
:ive 0; Mismatches 0;
                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="teaxon:9606"
/clone="NTZRP3003711"
/cell_type="teratocarcinoma"
/cell_line="NTZ"
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/organism="Homo sapiens"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
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Best Local Similarity
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT 13 CA415315

ORGANISM

AUTHORS TITLE

JOURNAL

COMMENT

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AU129261 AU128261 NT2RP2 Homo sapiens cDNA clone NT2RP2005190 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="neurula"
/lab_host="Bscherichia coli DH10B"
/clone_lib="xGC-neurula"
/note="vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."
                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mambhia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae, Xenopodinae, Silurana.

1 (bases 1 to 678)

Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
  AL650594 XGC-neurula Silurana tropicalis cDNA clone TNeu028f22 5'
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 550)
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Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.

CDNA was oligo dT primed from Sug of poly A+ RNA from neurula. BCORI-Notl cut cDNA was then ligated into pCS107 with BCORI at 5' end and Notl at the 3' end.

Vector: pCS107; Site 1: EcoRI; Site 2: Not!

Host: Escherichia coli pH108
                                                                                                                                                                                                                                                                                                                        On Dec 13, 2001 this sequence version replaced gi:17660265.
Concact: Huckle E
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 th 18.0%; Score 44; DB 9; Length 678; Similarity 72.0%; Pred. No. 0.86; 72; Conservative 0; Mismatches 25; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TNeu028f22.plkSP6
Sequencing primer: $P6.
Location/Qualifiers
                                                                                                                 Silurana tropicalis (western clawed frog)
Silurana tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'organism="Silurana tropicalis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TNeu028f22"
                                                                   AL650594.2 GI:38223211
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                          MRNA sequence.
AL650594
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The following repetitive elements were found in this cDNA sequence: 1-43, >POLY A#Simple_repeat (matched compliment) 413-491, SGC primer: M13 FORWARD
POLYA=YES.
                                                              EST 07-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                       CA415315

Gold bp mRNA linear EST 07-NOV-UI-H-EZO-baw-j-13-0-UI.SI NCI CGAP Chl Homo sapiens cDNA clone UI-H-EZO-baw-j-13-0-UI 3', mRNA sequence.
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TAG_LIB=UI-H-EZ0
TAG_SEQ=ATCTAATATG"
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Pred. No. 0.6;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cocation/Qualifiers
                                                                                                                           CA415315
CA415315.1 GI:24777966
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1 Similarity 92.2%;
47; Conservative (
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Unpublished (1997)
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Isogai, T.

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HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarator, Chiba 292-0812, Japan
Tel: 81-438-52-3976
Fax: 81-438-52-3976
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17.6%; Score 43; DB 9; Length 550;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 43; Conservative 0; Mismatches 0; Indels
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